

EXPRESSED SEQUENCES OF *ARABIDOPSIS THALIANA*5 *CROSS-REFERENCE TO RELATED APPLICATION*

This application claims the benefit of U.S. Provisional Application 60/178,472
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FIELD OF INVENTION

10 The invention is in the field of polynucleotide sequences of a plant, particularly
sequences expressed in *arabidopsis thaliana*.

BACKGROUND OF THE INVENTION

Plants and plant products have vast commercial importance in a wide variety of
areas including food crops for human and animal consumption, flavor enhancers for
15 food, and production of specialty chemicals for use in products such as medicaments
and fragrances. In considering food crops for humans and livestock, genes such as
those involved in a plant's resistance to insects, plant viruses, and fungi; genes involved
in pollination; and genes whose products enhance the nutritional value of the food, are
of major importance. A number of such genes have been described, see, for example,
20 McCaskill and Croteau (1999) *Nature Biotechnol.* 17:31-36.

Despite recent advances in methods for identification, cloning, and
characterization of genes, much remains to be learned about plant physiology in
general, including how plants produce many of the above-mentioned products;
mechanisms for resistance to herbicides, insects, plant viruses, fungi; elucidation of
25 genes involved in specific biosynthetic pathways; and genes involved in environmental
tolerance, e.g., salt tolerance, drought tolerance, or tolerance to anaerobic conditions.

Arabidopsis thaliana is a model system for genetic, molecular and biochemical
studies of higher plants. Features of this plant that make it a model system for genetic
and molecular biology research include a small genome size, organized into five
30 chromosomes and containing an estimated 20,000 genes, a rapid life cycle, prolific seed
production and, since it is small, it can easily be cultivation in limited space. *A. thaliana*

is a member of the mustard family (*Brassicaceae*) with a broad natural distribution throughout Europe, Asia, and North America. Many different ecotypes have been collected from natural populations and are available for experimental analysis. The entire life cycle, including seed germination, formation of a rosette plant, bolting of the main stem, flowering, and maturation of the first seeds, is completed in 6 weeks. A large number of mutant lines are available that affect nearly all aspects of its growth. These features greatly facilitate the isolation of fundamentally interesting and potentially important genes for agronomic development

Most gene products from higher plants exhibit adequate sequence similarity to deduced amino acid sequences of other plant genes to permit assignment of probable gene function, if it is known, in any higher plant. It is likely that there will be very few protein-encoding angiosperm genes that do not have orthologs or paralogs in *Arabidopsis*. The developmental diversity of higher plants may be largely due to changes in the cis-regulatory sequences of transcriptional regulators and not in coding sequences.

Many advances reported over the past few years offer clear evidence that this plant is not only a very important model species for basic research, but also extremely valuable for applied plant scientists and plant breeders. Knowledge gained from *Arabidopsis* can be used directly to develop desired traits in plants of other species.

Relevant Literature

Cold Spring Harbor Monograph 27 (1994) E.M. Meyerowitz and C.R. Somerville, eds. (CSH Laboratory Press). Annual Plant Reviews, Vol. 1: *Arabidopsis* (1998) M. Anderson and J.A. Roberts, eds. (CRC Press). Methods in Molecular Biology: *Arabidopsis* Protocols, Vol. 82 (1997) J.M. Martinez-Zapater and J. Salinas, eds. (CRC Press).

Mayer *et al* (1999) Nature **402**(6763):769-77; "Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*". Lin *et al.* (1999) **402**(6763):761-8, "Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*". Meinke *et al.* (1998) Science **282**:662-682, "*Arabidopsis thaliana*: a model plant for genome analysis". Somerville and Somerville (1999) Science **285**:380-383, "Plant functional

genomics". Mozo *et al.* (1999) Nat. Genet. **22**:271-275, "A complete BAC-based physical map of the *Arabidopsis thaliana* genome".

SUMMARY OF THE INVENTION

5 Novel nucleic acid sequences of *Arabidopsis thaliana*, their encoded polypeptides and variants thereof, genes corresponding to these nucleic acids, and proteins expressed by the genes, are provided.

 The invention also provides diagnostic, prophylactic and therapeutic agents employing such novel nucleic acids, their corresponding genes or gene products,
10 including expression constructs, probes, antisense constructs, and the like. The genetic sequences may also be used for the genetic manipulation of plant cells, particularly dicotyledonous plants. The encoded gene products and modified organisms are useful for introducing or improving disease resistance and stress tolerance into plants; screening of biologically active agents, *e.g.* fungicides, *etc.*; for elucidating biochemical
15 pathways; and the like.

 In one embodiment of the invention, a nucleic acid is provided that comprises a start codon; an optional intervening sequence; a coding sequence capable of hybridizing under stringent conditions as set forth in SEQ ID NO:1 to 999; and an optional terminal
20 sequence, wherein at least one of said optional sequences is present. Such a nucleic acid may correspond to naturally occurring *Arabidopsis* expressed sequences.

DETAILED DESCRIPTION OF THE INVENTION

 Novel nucleic acid sequences from *Arabidopsis thaliana*, their encoded polypeptides and variants thereof, genes corresponding to these nucleic acids and
25 proteins expressed by the genes are provided. The invention also provides agents employing such novel nucleic acids, their corresponding genes or gene products, including expression constructs, probes, antisense constructs, and the like. The nucleotide sequences are provided in the attached SEQLIST.

 Sequences include, but are not limited to, sequences that encode resistance
30 proteins; sequences that encode tolerance factors; sequences encoding proteins or other factors that are involved, directly or indirectly in biochemical pathways such as

metabolic or biosynthetic pathways, sequences involved in signal transduction, sequences involved in the regulation of gene expression, structural genes, and the like.

Biosynthetic pathways of interest include, but are not limited to, biosynthetic pathways whose product (which may be an end product or an intermediate) is of commercial, nutritional, or medicinal value.

The sequences may be used in screening assays of various plant strains to determine the strains that are best capable of withstanding a particular disease or environmental stress. Sequences encoding activators and resistance proteins may be introduced into plants that are deficient in these sequences. Alternatively, the sequences may be introduced under the control of promoters that are convenient for induction of expression. The protein products may be used in screening programs for insecticides, fungicides and antibiotics to determine agents that mimic or enhance the resistance proteins. Such agents may be used in improved methods of treating crops to prevent or treat disease. The protein products may also be used in screening programs to identify agents which mimic or enhance the action of tolerance factors. Such agents may be used in improved methods of treating crops to enhance their tolerance to environmental stresses.

Still other embodiments of the invention provide methods for enhancing or inhibiting production of a biosynthetic product in a plant by introducing a nucleic acid of the invention into a plant cell, where the nucleic acid comprises sequences encoding a factor which is involved, directly or indirectly in a biosynthetic pathway whose products are of commercial, nutritional, or medicinal value include any factor, usually a protein or peptide, which regulates such a biosynthetic pathway; which is an intermediate in such a biosynthetic pathway; or which in itself is a product that increases the nutritional value of a food product; or which is a medicinal product; or which is any product of commercial value.

Transgenic plants containing the antisense nucleic acids of the invention are useful for identifying other mediators that may induce expression of proteins of interest; for establishing the extent to which any specific insect and/or pathogen is responsible for damage of a particular plant; for identifying other mediators that may enhance or induce tolerance to environmental stress; for identifying factors involved in biosynthetic

pathways of nutritional, commercial, or medicinal value; or for identifying products of nutritional, commercial, or medicinal value.

In still other embodiments, the invention provides transgenic plants constructed by introducing a subject nucleic acid of the invention into a plant cell, and growing the cell into a callus and then into a plant; or, alternatively by breeding a transgenic plant from the subject process with a second plant to form an F1 or higher hybrid. The subject transgenic plants and progeny are used as crops for their enhanced disease resistance, enhanced traits of interest, for example size or flavor of fruit, length of growth cycle, *etc.*, or for screening programs, *e.g.* to determine more effective insecticides, *etc.* used as crops which exhibit enhanced tolerance environmental stress; or used to produce a factor.

Those skilled in the art will recognize the agricultural advantages inherent in plants constructed to have either increased or decreased expression of resistance proteins; or increased or decreased tolerance to environmental factors; or which produce or over-produce one or more factors involved in a biosynthetic pathway whose product is of commercial, nutritional, or medicinal value. For example, such plants may have increased resistance to attack by predators, insects, pathogens, microorganisms, herbivores, mechanical damage and the like; may be more tolerant to environmental stress, *e.g.* may be better able to withstand drought conditions, freezing, and the like; or may produce a product not normally made in the plant, or may produce a product in higher than normal amounts, where the product has commercial, nutritional, or medicinal value. Plants which may be useful include dicotyledons and monocotyledons.

Representative examples of plants in which the provided sequences may be useful include tomato, potato, tobacco, cotton, soybean, alfalfa, rape, and the like.

Monocotyledons, more particularly grasses (*Poaceae* family) of interest, include, without limitation, *Avena sativa* (oat); *Avena strigosa* (black oat); *Elymus* (wild rye); *Hordeum sp.* including *Hordeum vulgare* (barley); *Oryza sp.*, including *Oryza glaberrima* (African rice); *Oryza longistaminata* (long-staminate rice); *Pennisetum americanum* (pearl millet); *Sorghum sp.* (sorghum); *Triticum sp.*, including *Triticum aestivum* (common wheat); *Triticum durum* (durum wheat); *Zea mays* (corn); *etc.*

NUCLEIC ACID COMPOSITIONS

The following detailed description describes the nucleic acid compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these nucleic acids and genes; identification of structural motifs of the nucleic acids and genes; identification of the function of a gene product encoded by a gene corresponding to a nucleic acid of the invention; use of the provided nucleic acids as probes, in mapping, and in diagnosis; use of the corresponding polypeptides and other gene products to raise antibodies; use of the nucleic acids in genetic modification of plant and other species; and use of the nucleic acids, their encoded gene products, and modified organisms, for screening and diagnostic purposes.

The scope of the invention with respect to nucleic acid compositions includes, but is not necessarily limited to, nucleic acids having a sequence set forth in any one of SEQ ID NOS:1-999; nucleic acids that hybridize the provided sequences under stringent conditions; genes corresponding to the provided nucleic acids; variants of the provided nucleic acids and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product.

In one embodiment, the sequences of the invention provide a polypeptide coding sequence. The polypeptide coding sequence may correspond to a naturally expressed mRNA in Arabidopsis or other species, or may encode a fusion protein between one of the provided sequences and an exogenous protein coding sequence. The coding sequence is characterized by an ATG start codon, a lack of stop codons in-frame with the ATG, and a termination codon, that is, a continuous open frame is provided between the start and the stop codon. The sequence contained between the start and the stop codon will comprise a sequence capable of hybridizing under stringent conditions to a sequence set for in SEQ ID NO:1-999, and may comprise the sequence set forth in the Seqlist.

Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.

The invention features nucleic acids that are derived from *Arabidopsis thaliana*. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of SEQ ID NOS:1-999 or an identifying sequence thereof.

An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a nucleic acid sequence, e.g., exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOS:1-999.

The nucleic acids of the invention also include nucleic acids having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M NaCl/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM NaCl/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided nucleic acid sequences, e.g. allelic variants, genetically altered versions of the gene, etc., bind to the provided nucleic acid sequences (SEQ ID NOS:1-999) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, particularly grasses as previously described.

Preferably, hybridization is performed using at least 15 contiguous nucleotides of at least one of SEQ ID NOS:1-999. The probe will preferentially hybridize with a nucleic acid or mRNA comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes of more than 15 nucleotides can be used, e.g. probes of from about 18 nucleotides up to the entire length of the provided nucleic acid sequences, but 15 nucleotides generally represents sufficient sequence for unique identification.

The nucleic acids of the invention also include naturally occurring variants of the nucleotide sequences, e.g. degenerate variants, allelic variants, etc. Variants of the nucleic acids of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent
5 conditions. For example, by using appropriate wash conditions, variants of the nucleic acids of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair mismatches relative to the selected nucleic acid probe. In general, allelic variants contain 5-25% base pair mismatches, and can contain as little as even 2-5%, or 1-2% base pair mismatches, as well as a single base-pair mismatch.

10 The invention also encompasses homologs corresponding to the nucleic acids of SEQ ID NOS:1-999, where the source of homologous genes can be any related species, usually within the same genus or group. Homologs have substantial sequence similarity, e.g. at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a
15 reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, etc. A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., J. Mol. Biol. (1990)
20 215:403-10.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular).
25 For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Wateman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extention penalty,

30 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein. The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, etc., including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kb or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject expressed polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, etc. Isolated nucleic acids and nucleic acid fragments of the invention comprise at least about 15 up to about 100 contiguous nucleotides, or up to the complete sequence provided in SEQ ID NOS:1-999. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more.

Probes specific to the nucleic acids of the invention can be generated using the nucleic acid sequences disclosed in SEQ ID NOS:1-999 and the fragments as described above. The probes can be synthesized chemically or can be generated from longer nucleic acids using restriction enzymes. The probes can be labeled, for example, with

a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a nucleic acid of one of SEQ ID NOS:1-999. More preferably, probes are designed based on a contiguous sequence of one of the subject nucleic acids that remain unmasked following application of a masking program for
5 masking low complexity (e.g., XBLAST) to the sequence., *i.e.* one would select an unmasked region, as indicated by the nucleic acids outside the poly-n stretches of the masked sequence produced by the masking program.

The nucleic acids of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the nucleic acids, either
10 as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", e.g., flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The nucleic acids of the invention can be provided as a linear molecule or within
15 a circular molecule. They can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. They can be regulated by their own or by other regulatory sequences, as is known in the art. The nucleic acids of the invention can be introduced into suitable host cells using a variety of techniques which are available in the art, such as transferrin polycation-mediated DNA transfer,
20 transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological
25 samples, *e.g.* extracts of cells, to generate additional copies of the nucleic acids, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the nucleic acid sequences as shown in SEQ ID NOS:1-999 or variants thereof in a sample. These and other uses are
30 described in more detail below.

USE OF NUCLEIC ACIDS AS CODING SEQUENCES

Naturally occurring Arabidopsis polypeptides or fragments thereof are encoded by the provided nucleic acids. Methods are known in the art to determine whether the complete native protein is encoded by a candidate nucleic acid sequence. Where the provided sequence encodes a fragment of a polypeptide, methods known in the art may be used to determine the remaining sequence. These approaches may utilize a bioinformatics approach, a cloning approach, extension of mRNA species, *etc.*

Substantial genomic sequence is available for Arabidopsis, and may be exploited for determining the complete coding sequence corresponding to the provided sequences. The region of the chromosome to which a given sequence is located may be determined by hybridization or by database searching. The genomic sequence is then searched upstream and downstream for the presence of intron/exon boundaries, and for motifs characteristic of transcriptional start and stop sequences, for example by using Genscan (Burge and Karlin (1997) J. Mol. Biol. **268**:78-94); or GRAIL (Uberbacher and Mural (1991) P.N.A.S. **88**:11261-1265).

Alternatively, nucleic acid having a sequence of one of SEQ ID NOS:1-999, or an identifying fragment thereof, is used as a hybridization probe to complementary molecules in a cDNA library using probe design methods, cloning methods, and clone selection techniques as known in the art. Libraries of cDNA are made from selected cells. The cells may be those of *A. thaliana*, or of related species. In some cases it will be desirable to select cells from a particular stage, *e.g.* seeds, leaves, infected cells, *etc.*

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY; and Current Protocols in Molecular Biology, (1987 and updates) Ausubel et al., eds. The cDNA can be prepared by using primers based on sequence from SEQ ID NOS:1-999. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided nucleic acids, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection

experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (PCR Protocols: A Guide to Methods and Applications, (1990) Academic Press, Inc.) may be performed.

Genomic DNA is isolated using the provided nucleic acids in a manner similar to the isolation of full-length cDNAs. Briefly, the provided nucleic acids, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the nucleic acids of the invention, but this is not essential. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook et al., 9.4-9.30. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook *et al.*, such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

PCR methods may be used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant nucleic acids. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, is used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the nucleic acid sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al.*, WO 95/04745 and Gruber *et al.*, U.S. Pat. No. 5,500,356.

Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

“Rapid amplification of cDNA ends”, or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the instant nucleic acids, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA.

A description of this methods is reported in WO 97/19110. A common primer may be designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends. When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook et al., 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function. As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more nucleic acids of the invention can be synthesized.

EXPRESSION OF POLYPEPTIDES

The provided nucleic acid, e.g. a nucleic acid having a sequence of one of SEQ ID NOS:1-999), the corresponding cDNA, the polypeptide coding sequence as described above, or the full-length gene is used to express a partial or complete gene product. Constructs of nucleic acids having sequences of SEQ ID NOS:1-999 can be generated by recombinant methods, synthetically, or in a single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, e.g. Stemmer *et al.*, Gene (Amsterdam) (1995) 164(1):49-53.

Appropriate nucleic acid constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY.

The gene product encoded by a nucleic acid of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems.

The subject nucleic acid molecules are generally propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole organism or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially.

The nucleic acids set forth in SEQ ID NOS:1-999 or their corresponding full-length nucleic acids are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters attached either at the 5' end of the sense strand or at the 3' end of the antisense strand, enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive.

In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the nucleic acids or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

IDENTIFICATION OF FUNCTIONAL AND STRUCTURAL MOTIFS

Translations of the nucleotide sequence of the provided nucleic acids, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the nucleic acids of the invention. Also, sequences exhibiting similarity with more than one

individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The six possible reading frames may be translated using programs such as GCG pepdata, or GCG Frames (Wisconsin Package Version 10.0, Genetics Computer Group (GCG) , Madison, Wisconsin, USA.). Programs such as ORFFinder (National Center for Biotechnology Information (NCBI) a division of the National Library of Medicine (NLM) at the National Institutes of Health (NIH) <http://www.ncbi.nlm.nih.gov/>) may be used to identify open reading frames (ORFs) in sequences. ORF finder identifies all possible ORFs in a DNA sequence by locating the standard and alternative stop and start codons. Other ORF identification programs include Genie (Kulp *et al.* (1996).

A generalized Hidden Markov Model may be used for the recognition of genes in DNA. (ISMB-96, St. Louis, MO, AAAI/MIT Press; Reese *et al.* (1997), "Improved splice site detection in Genie". Proceedings of the First Annual International Conference on Computational Molecular Biology RECOMB 1997, Santa Fe, NM, ACM Press, New York., P. 34.); BESTORF --Prediction of potential coding fragment in human or plant EST/mRNA sequence data using Markov Chain Models; and FGENEP -- Multiple genes structure prediction in plant genomic DNA (Solovyev *et al.* (1995) Identification of human gene structure using linear discriminant functions and dynamic programming. In Proceedings of the Third International Conference on Intelligent Systems for Molecular Biology eds. Rawling *et al.* Cambridge, England, AAAI Press,367-375.; Solovyev *et al.* (1994) Nucl. Acids Res. **22**(24):5156-5163; Solovyev *et al.*, The prediction of human exons by oligonucleotide composition and discriminant analysis of spliceable open reading frames, in: The Second International conference on Intelligent systems for Molecular Biology (eds. Altman *et al.*), AAAI Press, Menlo Park, CA (1994, 354-362) Solovyev and Lawrence, Prediction of human gene structure using dynamic programming and oligonucleotide composition, In: Abstracts of the 4th annual Keck symposium. Pittsburgh, 47,1993; Burge and Karlin (1997) J. Mol. Biol. **268**:78-94; Kulp *et al.* (1996) Proc. Conf. on Intelligent Systems in Molecular Biology '96, 134-142).

The full length sequences and fragments of the nucleic acid sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided nucleic acids. Typically, a selected nucleic

acid is translated in all six frames to determine the best alignment with the individual sequences. These amino acid sequences are referred to, generally, as query sequences, which are aligned with the individual sequences. Suitable databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

- 5 Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available by ftp at <ftp://ncbi.nlm.nih.gov/>.

- Gapped BLAST and PSI-BLAST are useful search tools provided by NCBI. (version 2.0) (Altschul *et al.*, 1997). Position-Specific Iterated BLAST (PSI-BLAST)
10 provides an automated, easy-to-use version of a "profile" search, which is a sensitive way to look for sequence homologues. The program first performs a gapped BLAST database search. The PSI-BLAST program uses the information from any significant alignments returned to construct a position-specific score matrix, which replaces the query sequence for the next round of database searching. PSI-BLAST may be iterated
15 until no new significant alignments are found. The Gapped BLAST algorithm allows gaps (deletions and insertions) to be introduced into the alignments that are returned. Allowing gaps means that similar regions are not broken into several segments. The scoring of these gapped alignments tends to reflect biological relationships more closely. The Smith-Waterman is another algorithm that produces local or global gapped
20 sequence alignments, see Meth. Mol. Biol. (1997) 70: 173-187. Also, the GAP program using the Needleman and Wunsch global alignment method can be utilized for sequence alignments.

- Results of individual and query sequence alignments can be divided into three categories, high similarity, weak similarity, and no similarity. Individual alignment results
25 ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and e value.

- The percentage of the alignment region length is calculated by counting the
30 number of residues of the individual sequence found in the region of strongest alignment, e.g. contiguous region of the individual sequence that contains the greatest

number of residues that are identical to the residues of the corresponding region of the aligned query sequence. This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11 amino acid stretch. The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%

E value is the probability that the alignment was produced by chance. For a single alignment, the e value can be calculated according to Karlin et al., Proc. Natl. Acad. Sci. (1990) 87:2264 and Karlin et al., Proc. Natl. Acad. Sci. (1993) 90. The e value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul et al., Nat. Genet. (1994) 6:119. Alignment programs such as BLAST program can calculate the e value.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, *supra*; BLAST or FASTA programs; or by determining the area where sequence identity is highest.

In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the

alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. The query sequence is considered to have a high similarity with a profile sequence when the p value is less than or equal to 10^{-2} . Confidence in the degree of similarity between the query sequence and the profile sequence increases as the p value become smaller.

In general, where alignment results considered to be of weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically; at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues. Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

The query sequence is considered to have a low similarity with a profile sequence when the p value is greater than 10^{-2} . Confidence in the degree of similarity between the query sequence and the profile sequence decreases as the p values become larger.

Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a

measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

It is apparent, when studying protein sequence families, that some regions have been better conserved than others during evolution. These regions are generally important for the function of a protein and/or for the maintenance of its three-dimensional structure. By analyzing the constant and variable properties of such groups of similar sequences, it is possible to derive a signature for a protein family or domain, which distinguishes its members from all other unrelated proteins. A pertinent analogy is the use of fingerprints by the police for identification purposes. A fingerprint is generally sufficient to identify a given individual. Similarly, a protein signature can be used to assign a new sequence to a specific family of proteins and thus to formulate hypotheses about its function. The PROSITE database is a compendium of such fingerprints (motifs) and may be used with search software such as Wisconsin GCG Motifs to find motifs or fingerprints in query sequences. PROSITE currently contains signatures specific for about a thousand protein families or domains. Each of these signatures comes with documentation providing background information on the structure and function of these proteins (Hofmann *et al.* (1999) Nucleic Acids Res. **27**:215-219; Bucher and Bairoch ., A generalized profile syntax for biomolecular sequences motifs and its function in automatic sequence interpretation (In) ISMB-94; Proceedings 2nd International Conference on Intelligent Systems for Molecular Biology; Altman *et al.* Eds. (1994), pp 53-61, AAAI Press, Menlo Park).

Translations of the provided nucleic acids can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided nucleic acids can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene

products (e.g., polypeptides) encoded by the provided nucleic acids or corresponding cDNA or genes.

Profiles can be designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney et al., *Nucl. Acid Res.* (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are available for downloading to a local server. For example, the PFAM database with MSAs of 547 different families and motifs, and the software (HMMER) to search the PFAM database may be downloaded from <ftp://ftp.genetics.wustl.edu/pub/eddy/pfam-4.4/> to allow secure searches on a local server. Pfam is a database of multiple alignments of protein domains or conserved protein regions., which represent evolutionary conserved structure that has implications for the protein's function (Sonnhammer et al. (1998) *Nucl. Acid Res.* **26**:320-322; Bateman et al. (1999) *Nucleic Acids Res.* **27**:260-262).

The 3D_al_i databank (Pasarella, S. and Argos, P. (1992) *Prot. Engineering* 5:121-137) was constructed to incorporate new protein structural and sequence data. The databank has proved useful in many research fields such as protein sequence and structure analysis and comparison, protein folding, engineering and design and evolution. The collection enhances present protein structural knowledge by merging information from proteins of similar main-chain fold with homologous primary structures taken from large databases of all known sequences. 3D_al_i databank files may be downloaded to a secure local server from http://www.embl-heidelberg.de/argos/ali/ali_form.html.

The identify and function of the gene that correlates to a nucleic acid described herein can be determined by screening the nucleic acids or their corresponding amino acid sequences against profiles of protein families. Such profiles focus on common structural motifs among proteins of each family. Publicly available profiles are known in the art.

In comparing a novel nucleic acid with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng et al., *J. Mol. Evol.* (1987) 25:351. Another method, GAP,

uses the alignment method of Needleman et al., J. Mol. Biol. (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith *et al.* (1981) Adv. Appl. Math. 2:482.

5

IDENTIFICATION OF SECRETED & MEMBRANE-BOUND POLYPEPTIDES

Secreted and membrane-bound polypeptides of the present invention are of interest. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides. A signal sequence is usually encoded by
10 both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a
15 stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, Proc. Natl. Acad. Sci. USA (1981) 78:3824-3828; Kyte & Doolittle, J. Mol. Biol. (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti et al., Eur. J.
20 Biochem. (1990) 190: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the nucleic acids of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino
25 acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine.

IDENTIFICATION OF THE FUNCTION OF AN EXPRESSION PRODUCT

30 The biological function of the encoded gene product of the invention may be determined by empirical or deductive methods. One promising avenue, termed

phylogenomics, exploits the use of evolutionary information to facilitate assignment of gene function. The approach is based on the idea that functional predictions can be greatly improved by focusing on how genes became similar in sequence during evolution instead of focusing on the sequence similarity itself. One of the major efficiencies that has emerged from plant genome research to date is that a large percentage of higher plant genes can be assigned some degree of function by comparing them with the sequences of genes of known function.

Alternatively, "reverse genetics" is used to identify gene function. Large collections of insertion mutants are available for *Arabidopsis*, maize, petunia, and snapdragon. These collections can be screened for an insertional inactivation of any gene by using the polymerase chain reaction (PCR) primed with oligonucleotides based on the sequences of the target gene and the insertional mutagen. The presence of an insertion in the target gene is indicated by the presence of a PCR product. By multiplexing DNA samples, hundreds of thousands of lines can be screened and the corresponding mutant plants can be identified with relatively small effort. Analysis of the phenotype and other properties of the corresponding mutant will provide an insight into the function of the gene.

In one method of the invention, the gene function in a transgenic *Arabidopsis* plant is assessed with anti-sense constructs. A high degree of gene duplication is apparent in *Arabidopsis*, and many of the gene duplications in *Arabidopsis* are very tightly linked. Large numbers of transgenic *Arabidopsis* plants can be generated by infecting flowers with *Agrobacterium tumefaciens* containing an insertional mutagen, a method of gene silencing based on producing double-stranded RNA from bidirectional transcription of genes in transgenic plants can be broadly useful for high-throughput gene inactivation (Clough and Bent (1999) Plant J. **17**; Waterhouse *et al.* (1998) Proc. Natl. Acad. Sci. U.S.A. **95**:13959). This method may use promoters that are expressed in only a few cell types or at a particular developmental stage or in response to an external stimulus. This could significantly obviate problems associated with the lethality of some mutations.

Virus-induced gene silencing may also find use for suppressing gene function. This method exploits the fact that some or all plants have a surveillance system that

can specifically recognize viral nucleic acids and mount a sequence-specific suppression of viral RNA accumulation. By inoculating plants with a recombinant virus containing part of a plant gene, it is possible to rapidly silence the endogenous plant gene.

5 Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense nucleic acids based on a selected nucleic acid sequence can interfere with expression of the corresponding gene. Antisense nucleic acids are typically generated within the cell by expression from
10 antisense constructs that contain the antisense strand as the transcribed strand. Antisense nucleic acids based on the disclosed nucleic acids will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense nucleic acid. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene
15 corresponding to the nucleic acid upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

As an alternative method for identifying function of the gene corresponding to a nucleic acid disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will
20 interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield
25 dominant negative mutants. General strategies are available for making dominant negative mutants (see for example, Herskowitz (1987) Nature 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

Another approach for discovering the function of genes utilizes gene chips and
30 microarrays. DNA sequences representing all the genes in an organism can be placed on miniature solid supports and used as hybridization substrates to quantitate the

expression of all the genes represented in a complex mRNA sample. This information is used to provide extensive databases of quantitative information about the degree to which each gene responds to pathogens, pests, drought, cold, salt, photoperiod, and other environmental variation. Similarly, one obtains extensive information about which genes respond to changes in developmental processes such as germination and flowering. One can therefore determine which genes respond to the phytohormones, growth regulators, safeners, herbicides, and related agrichemicals. These databases of gene expression information provide insights into the "pathways" of genes that control complex responses. The accumulation of DNA microarray or gene chip data from many different experiments creates a powerful opportunity to assign functional information to genes of otherwise unknown function. The conceptual basis of the approach is that genes that contribute to the same biological process will exhibit similar patterns of expression. Thus, by clustering genes based on the similarity of their relative levels of expression in response to diverse stimuli or developmental or environmental conditions, it is possible to assign functions to many genes based on the known function of other genes in the cluster.

CONSTRUCTION OF POLYPEPTIDES OF THE INVENTION AND VARIANTS THEREOF

The polypeptides of the invention include those encoded by the disclosed nucleic acids. These polypeptides can also be encoded by nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed nucleic acids. Thus, the invention includes within its scope a polypeptide encoded by a nucleic acid having the sequence of any one of SEQ ID NOS: 1-999 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited nucleic acid, the polypeptide encoded by the gene represented by the recited nucleic acid, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein.

In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a

differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, i.e., the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

5 In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, e.g. are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that
10 is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions,
15 additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general
20 charge, hydrophobicity/hydrophilicity, and/or steric bulk of the amino acid substituted.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 amino acids (aa) to at least about
15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a nucleic acid having a sequence of any SEQ ID NOS:1-999, or a homolog thereof.
25

The protein variants described herein are encoded by nucleic acids that are within the scope of the invention. The genetic code can be used to select the
30 appropriate codons to construct the corresponding variants.

LIBRARIES AND ARRAYS

In general, a library of biopolymers is a collection of sequence information, which information is provided in either biochemical form (e.g., as a collection of nucleic acid or polypeptide molecules), or in electronic form (e.g., as a collection of genetic sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The term biopolymer, as used herein, is intended to refer to polypeptides, nucleic acids, and derivatives thereof, which molecules are characterized by the possession of genetic sequences either corresponding to, or encoded by, the sequences set forth in the provided sequence list (seqlist). The sequence information can be used in a variety of ways, e.g., as a resource for gene discovery, as a representation of sequences expressed in a selected cell type, e.g. cell type markers, etc.

The nucleic acid libraries of the subject invention include sequence information of a plurality of nucleic acid sequences, where at least one of the nucleic acids has a sequence of any of SEQ ID NOS:1-999. By plurality is meant one or more, usually at least 2 and can include up to all of SEQ ID NOS:1-999. The length and number of nucleic acids in the library will vary with the nature of the library, e.g., if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the sequences or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, e.g. the nucleic acid sequences of any of the nucleic acids of SEQ ID NOS:1-999, can be recorded on computer readable media, e.g. any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the

art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, e.g. word processing text file, database format, etc. In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (e.g., searchable files, executable files, etc, including, but not limited to, for example, search program software, etc.)

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul et al., supra.) and BLAZE (Brutlag et al. Comp. Chem. (1993) 17:203) search algorithms on a Sybase system can be used identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif with the stored sequence information. Search means are used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, e.g. MacPattern

(EMBL), BLASTN, BLASTX (NCBI) and tBLASTX. A "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues.

5 A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme
10 active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

 A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present
15 invention. One format for an output means ranks fragments of the genome possessing varying degrees of homology to a target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences and identifies the degree of sequence similarity contained in the identified fragment.

 A variety of comparing means can be used to compare a target sequence or
20 target motif with the data storage means to identify sequence fragments of the genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention.

 As discussed above, the "library" of the invention also encompasses biochemical
25 libraries of the nucleic acids of SEQ ID NOS:1-999, e.g., collections of nucleic acids representing the provided nucleic acids. The biochemical libraries can take a variety of forms, e.g. a solution of cDNAs, a pattern of probe nucleic acids stably bound to a surface of a solid support (microarray) and the like. By array is meant an article of manufacture that has a solid support or substrate with one or more nucleic acid targets
30 on one of its surfaces, where the number of distinct nucleic may be in the hundreds, thousand, or tens of thousands. Each nucleic acid will comprise at 18 nt and often at

least 25 nt, and often at least 100 to 1000 nucleotides, and may represent up to a complete coding sequence or cDNA.. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOS:1-999.

GENETICALLY ALTERED CELLS AND TRANSGENICS

The subject nucleic acids can be used to create genetically modified and transgenic organisms, usually plant cells and plants, which may be monocots or dicots.

The term transgenic, as used herein, is defined as an organism into which an exogenous nucleic acid construct has been introduced, generally the exogenous sequences are stably maintained in the genome of the organism. Of particular interest are transgenic organisms where the genomic sequence of germ line cells has been stably altered by introduction of an exogenous construct.

Typically, the transgenic organism is altered in the genetic expression of the introduced nucleotide sequences as compared to the wild-type, or unaltered organism.

For example, constructs that provide for over-expression of a targeted sequence, sometimes referred to as a "knock-in", provide for increased levels of the gene product.

Alternatively, expression of the targeted sequence can be down-regulated or substantially eliminated by introduction of a "knock-out" construct, which may direct transcription of an anti-sense RNA that blocks expression of the naturally occurring mRNA, by deletion of the genomic copy of the targeted sequence, *etc.*

In one method, large numbers of genes are simultaneously introduced in order to explore the genetic basis of complex traits, for example by making plant artificial chromosome (PLAC) libraries. The centromeres in *Arabidopsis* have been mapped and current genome sequencing efforts will extend through these regions. Because *Arabidopsis* telomeres are very similar to those in yeast one may use a hybrid sequence

of alternating plant and yeast sequences that function in both types of organisms, developing yeast artificial chromosome-PLAC libraries, and then introducing them into a suitable plant host to evaluate the phenotypic consequences. By providing a defined chromosomal environment for cloned genes, the use of PLACs may also enhance the ability to produce transgenic plants with defined levels of gene expression.

It has been found in many organisms that there is significant redundancy in the representation of genes in a genome. That is, a particular gene function is likely by represented by multiple copies of similar coding sequences in the genome. These copies are typically conserved in the amino acid sequence, but may diverge in the sequence of non-translated sequences, and in their codon usage. In order to knock out a particular genetic function in an organism, it may not be sufficient to delete a genomic copy of a single gene. In such cases it may be preferable to achieve a genetic knock-out with an anti-sense construct, particularly where the sequence is aligned with the coding portion of the mRNA.

Methods of transforming plant cells are well-known in the art, and include protoplast transformation, tungsten whiskers (Coffee et al., U.S. Pat. No. 5,302,523, issued Apr. 12, 1994), directly by microorganisms with infectious plasmids, use of transposons (U.S. Patent No. 5,792,294), infectious viruses, the use of liposomes, microinjection by mechanical or laser beam methods, by whole chromosomes or chromosome fragments, electroporation, silicon carbide fibers, and microprojectile bombardment.

For example, one may utilize the biolistic bombardment of meristem tissue, at a very early stage of development, and the selective enhancement of transgenic sectors toward genetic homogeneity, in cell layers that contribute to germline transmission.

Biolistics-mediated production of fertile, transgenic maize is described in Gordon-Kamm et al. (1990), Plant Cell 2:603; Fromm et al. (1990) Bio/Technology 8: 833, for example.

Alternatively, one may use a microorganism, including but not limited to, *Agrobacterium tumefaciens* as a vector for transforming the cells, particularly where the targeted plant is a dicotyledonous species. See, for example, U.S. Patent No. 5,635,381. Leung et al. (1990) Curr. Genet. 17(5):409-11 describe integrative transformation of three fertile

hermaphroditic strains of *Arabidopsis thaliana* using plasmids and cosmids that contain an *E. coli* gene linked to *Aspergillus nidulans* regulatory sequences.

Preferred expression cassettes for cereals may include promoters that are known to express exogenous DNAs in corn cells. For example, the Adh1 promoter has been shown to be strongly expressed in callus tissue, root tips, and developing kernels in corn. Promoters that are used to express genes in corn include, but are not limited to, a plant promoter such as the, CaMV 35S promoter (Odell et al., Nature, 313, 810 (1985)), or others such as CaMV 19S (Lawton et al., Plant Mol. Biol., 9, 31F (1987)), nos (Ebert et al., PNAS USA, 84, 5745 (1987)), Adh (Walker et al., PNAS USA, 84, 6624 (1987)), sucrose synthase (Yang et al., PNAS USA, 87, 4144 (1990)), .alpha.-tubulin, ubiquitin, actin (Wang et al., Mol. Cell. Biol., 12, 3399 (1992)), cab (Sullivan et al., Mol. Gen. Genet, 215, 431 (1989)), PEPCase (Hudspeth et al., Plant Mol. Biol., 12, 579 (1989)), or those associated with the R gene complex (Chandler et al., The Plant Cell, 1, 1175 (1989)). Other promoters useful in the practice of the invention are known to those of skill in the art.

Tissue-specific promoters, including but not limited to, root-cell promoters (Conkling et al., Plant Physiol., 93, 1203 (1990)), and tissue-specific enhancers (Fromm et al., The Plant Cell, 1, 977 (1989)) are also contemplated to be particularly useful, as are inducible promoters such as water-stress-, ABA- and turgor-inducible promoters (Guerrero et al., Plant Molecular Biology, 15, 11-26)), and the like.

Regulating and/or limiting the expression in specific tissues may be functionally accomplished by introducing a constitutively expressed gene (all tissues) in combination with an antisense gene that is expressed only in those tissues where the gene product is not desired. Expression of an antisense transcript of this preselected DNA segment in an rice grain, using, for example, a zein promoter, would prevent accumulation of the gene product in seed. Hence the protein encoded by the preselected DNA would be present in all tissues except the kernel.

Alternatively, one may wish to obtain novel tissue-specific promoter sequences for use in accordance with the present invention. To achieve this, one may first isolate cDNA clones from the tissue concerned and identify those clones which are expressed specifically in that tissue, for example, using Northern blotting or DNA microarrays.

Ideally, one would like to identify a gene that is not present in a high copy number, but which gene product is relatively abundant in specific tissues. The promoter and control elements of corresponding genomic clones may then be localized using the techniques of molecular biology known to those of skill in the art. Alternatively, promoter elements
5 can be identified using enhancer traps based on T-DNA and/or transposon vector systems (see, for example, Campisi *et al.* (1999) Plant J. **17**:699-707; Gu *et al.* (1998) Development **125**:1509-1517).

In some embodiments of the present invention expression of a DNA segment in a transgenic plant will occur only in a certain time period during the development of the
10 plant. Developmental timing is frequently correlated with tissue specific gene expression. For example, in corn expression of zein storage proteins is initiated in the endosperm about 15 days after pollination.

Ultimately, the most desirable DNA segments for introduction into a plant genome may be homologous genes or gene families which encode a desired trait (e.g.,
15 increased disease resistance) and which are introduced under the control of novel promoters or enhancers, etc., or perhaps even homologous or tissue-specific (e.g., root-, grain- or leaf-specific) promoters or control elements.

The genetically modified cells are screened for the presence of the introduced genetic material. The cells may be used in functional studies, drug screening, *etc.*, e.g.
20 to study chemical mode of action, to determine the effect of a candidate agent on pathogen growth, infection of plant cells, *etc.*

The modified cells are useful in the study of genetic function and regulation, for alteration of the cellular metabolism, and for screening compounds that may affect the biological function of the gene or gene product. For example, a series of small deletions
25 and/or substitutions may be made in the host's native gene to determine the role of different domains and motifs in the biological function. Specific constructs of interest include anti-sense, as previously described, which will reduce or abolish expression, expression of dominant negative mutations, and over-expression of genes.

Where a sequence is introduced, the introduced sequence may be either a
30 complete or partial sequence of a gene native to the host, or may be a complete or partial sequence that is exogenous to the host organism, e.g., an *A. thaliana* sequence

inserted into wheat plants. A detectable marker, such as *aldA*, *lac Z*, *etc.* may be introduced into the locus of interest, where upregulation of expression will result in an easily detected change in phenotype.

One may also provide for expression of the gene or variants thereof in cells or tissues where it is not normally expressed, at levels not normally present in such cells or tissues, or at abnormal times of development, during sporulation, *etc.* By providing expression of the protein in cells in which it is not normally produced, one can induce changes in cell behavior.

DNA constructs for homologous recombination will comprise at least a portion of the provided gene or of a gene native to the species of the host organism, wherein the gene has the desired genetic modification(s), and includes regions of homology to the target locus (see Kempin *et al.* (1997) Nature **389**:802-803). DNA constructs for random integration or episomal maintenance need not include regions of homology to mediate recombination. Conveniently, markers for positive and negative selection are included. Methods for generating cells having targeted gene modifications through homologous recombination are known in the art.

Embodiments of the invention provide processes for enhancing or inhibiting synthesis of a protein in a plant by introducing a provided nucleic acids sequence into a plant cell, where the nucleic acid comprises sequences encoding a protein of interest. For example, enhanced resistance to pathogens may be achieved by inserting a nucleic acid encoding an activator in a vector downstream from a promoter sequence capable of driving constitutive high-level expression in a plant cell. When grown into plants, the transgenic plants exhibit increased synthesis of resistance proteins, and increased resistance to pathogens.

Other embodiments of the invention provide processes for enhancing or inhibiting synthesis of a tolerance factor in a plant by introducing a nucleic acid of the invention into a plant cell, where the nucleic acid comprises sequences encoding a tolerance factor. For example, enhanced tolerance to an environmental stress may be achieved by inserting a nucleic acid encoding an activator in a vector downstream from a promoter sequence capable of driving constitutive high-level expression in a plant cell.

When grown into plants, the transgenic plants exhibit increased synthesis of tolerance proteins, and increased tolerance to environmental stress.

Factors which are involved, directly or indirectly in biosynthetic pathways whose products are of commercial, nutritional, or medicinal value include any factor, usually
5 a protein or peptide, which regulates such a biosynthetic pathway (e.g., an activator or repressor); which is an intermediate in such a biosynthetic pathway; or which is a product that increases the nutritional value of a food product; a medicinal product; or any product of commercial value and/or research interest. Plant and other cells may be genetically modified to enhance a trait of interest, by upregulating or down-regulating
10 factors in a biosynthetic pathway.

SCREENING ASSAYS

The polypeptides encoded by the provided nucleic acid sequences, and cells genetically altered to express such sequences, are useful in a variety of screening
15 assays to determine effect of candidate inhibitors, activators., or modifiers of the gene product. One may determine what insecticides, fungicides and the like have an enhancing or synergistic activity with a gene. Alternatively, one may screen for compounds that mimic the activity of the protein. Similarly, the effect of activating agents may be used to screen for compounds that mimic or enhance the activation of
20 proteins. Candidate inhibitors of a particular gene product are screened by detecting decreased from the targeted gene product.

The screening assays may use purified target macromolecules to screen large compound libraries for inhibitory drugs; or the purified target molecule may be used for a rational drug design program, which requires first determining the structure of the
25 macromolecular target or the structure of the macromolecular target in association with its customary substrate or ligand. This information is then used to design compounds which must be synthesized and tested further. Test results are used to refine the molecular models and drug design process in an iterative fashion until a lead compound emerges.

30 Drug screening may be performed using an *in vitro* model, a genetically altered cell, or purified protein. One can identify ligands or substrates that bind to, modulate or

mimic the action of the target genetic sequence or its product. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, and the like.

The purified protein may also be used for determination of three-dimensional crystal structure, which can be used for modeling intermolecular interactions.

Where the nucleic acid encodes a factor involved in a biosynthetic pathway, as described above, it may be desirable to identify factors, e.g., protein factors, which interact with such factors. One can identify interacting factors, ligands, substrates that bind to, modulate or mimic the action of the target genetic sequence or its product. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, and the like. *In vivo* assays for protein-protein interactions in *E. coli* and yeast cells are also well-established (see Hu *et al.* (2000) Methods **20**:80-94; and Bai and Elledge (1997) Methods Enzymol. **283**:141-156).

The purified protein may also be used for determination of three-dimensional crystal structure, which can be used for modeling intermolecular interactions. It may also be of interest to identify agents that modulate the interaction of a factor identified as described above with a factor encoded by a nucleic acid of the invention. Drug screening can be performed to identify such agents. For example, a labeled *in vitro* protein-protein binding assay can be used, which is conducted in the presence and absence of an agent being tested.

The term "agent" as used herein describes any molecule, e.g. protein or pharmaceutical, with the capability of altering or mimicking a physiological function. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, *i.e.* at zero concentration or below the level of detection.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen

bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides.

Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and organism extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries.

Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs.

Where the screening assay is a binding assay, one or more of the molecules may be joined to a label, where the label can directly or indirectly provide a detectable signal.

Various labels include radioisotopes, fluorescers, chemilumescers, enzymes, specific binding molecules, particles, *e.g.* magnetic particles, and the like. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin *etc.* For the specific binding members, the complementary member would normally be labeled with a molecule that provides for detection, in accordance with known procedures.

A variety of other reagents may be included in the screening assay. These include reagents like salts, neutral proteins, *e.g.* albumin, detergents, *etc.* that are used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Reagents that improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.* may be used. The mixture of components are added in any order that provides for the requisite binding. Incubations are performed at any suitable temperature, typically between 4 and 40° C. Incubation

periods are selected for optimum activity, but may also be optimized to facilitate rapid high-throughput screening. Typically between 0.1 and 1 hours will be sufficient.

5 The compounds having the desired biological activity may be administered in an acceptable carrier to a host. The active agents may be administered in a variety of ways. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.01-100 wt.%.

10 It must be noted that as used herein and in the appended claims, the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a complex" includes a plurality of such complexes and reference to "the formulation" includes reference to one or more formulations and equivalents thereof known to those skilled in the art, and so forth.

15 Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described.

20 All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing, for example, the methods and methodologies that are described in the publications which might be used in connection with the presently described invention. The publications discussed above and throughout the text are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention.

25

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the subject invention, and are not intended to limit the scope of what is regarded as the invention.

30 Efforts have been made to ensure accuracy with respect to the numbers used (e.g. amounts, temperature, concentrations, etc.) but some experimental errors and deviations should be allowed for. Unless otherwise indicated, parts are parts by weight,

molecular weight is average molecular weight, temperature is in degrees Celsius, and pressure is at or near atmospheric.

EXPERIMENTAL

5 Cloning and Characterization of *Arabidopsis thaliana* Genes.

Following DNA isolation, sequencing was performed using the Dye Primer Sequencing protocol, below. The sequencing reactions were loaded by hand onto a 48 lane ABI 377 and run on a 36 cm gel with the 36E-2400 run module and extraction. Gel analysis was performed with ABI software.

10 The Phred program was used to read the sequence trace from the ABI sequencer, call the bases and produce a sequence read and a quality score for each base call in the sequence., (Ewing *et al.* (1998) Genome Research 8:175-185; Ewing and Green (1998) Genome Research 8:186-194.) PolyPhred may be used to detect single nucleotide polymorphisms in sequences (Kwok *et al.* (1994) Genomics 25:615-
15 622; Nickerson *et al.* (1997) Nucleic Acids Research 25(14):2745-2751.)

MicroWave Plasmid Protocol: Fill Beckman 96 deep-well growth blocks with 1 ml of TB containing 50 µg of ampicillin per ml. Inoculate each well with a colony picked with a toothpick or a 96-pin tool from a glycerol stock plate. Cover the blocks with a plastic lid
20 and tape at two ends to hold lid in place. Incubate overnight (16-24 hours depending on the host stain) at 37° C with shaking at 275 rpm in a New Brunswick platform shaker. Pellet cells by centrifugation for 20 minutes at 3250 rpm in a Beckman GS-R6K, decant TB and freeze pelleted cell in the 96 well block. Thaw blocks on the bench when ready to continue.

25

Prepare the MW-Tween20 solution

For four blocks:

50ml STET/TWEEN20

30 2 tubes RNase (10mg/ml,600ulea)

1 tube lysozyme (25mg)

For 16 blocks:

200ml STET/TWEEN

8 tubes RNase

4 tubes lysozyme

Pipette RNase and Lysozyme into the corner of a beaker. Add Tween 20 solution and swirl to mix completely. Use the Multidrop (or Biohit) to add 25ul of sterile H₂O (from the L size autoclaved bottles) to each well. Resuspend the pellets by vortexing on setting 10 of the platform vortexer. Check pellets after 4 min. and repeat as necessary to resuspend completely. Use the multidrop to add 70 µl of the freshly prepared MW-Tween 20 solution to each well. Vortex at setting 6 on the platform vortex for 15 seconds. Do not cause frothing.

Incubate the blocks at room temperature for 5 min. Place two blocks at a time in the microwave (1000 Watts) with the tape (placed on the H1 to H12 side of the block) facing away from each other and turn on at full power for 30 seconds. Rotate the blocks so that the tapes face towards each other and turn on at full power again for 30 seconds.

Immediately remove the blocks from the microwave and add 300 µl of sterile ice cold H₂O with the Multidrop. Seal the blocks with foil tape and place them in an H₂O/ice bath.

Vortex the blocks on 5 for 15 seconds and leave them in the H₂O/Ice bath. Return to step 7 until all the blocks are in the ice water bath. Incubate the blocks for 15 minutes on ice. Spin the blocks for 30 minutes in the Beckman GS-6KR with GH3.8 rotor with Microplus carrier at 3250rpm.

Transfer 100 µl of the supernatant to Corning/Costar round bottom 96 well trays. Cover with foil and put into fridge if to be sequenced right away. If not to be sequenced in the next day, freeze them at -20° C.

Dye Primer Sequencing: Spin down the DP brew trays and DNA template by pulsing in the Beckman GS-6KR with GH3.8 rotor with Microplus carrier. Big Dye Primer reaction mix trays (one 96 well cycleplate (Robbins) for each nucleotide), 3 microliters of reaction mix per well.

Use twelve channel pipetter (Costar) to add 2 µl of template to one each G,A,T,C, trays for each template plate. Pulse again to get both the reaction mix and template into the bottom of the cycle plate and put them into the MJ Research DNA Tetrad (PTC-225).

Start program Dye-Primer. Dye-primer is:

96° C, 1 min 1 cycle

96° C, 10 sec.

55° C, 5 sec.

5 70° C, 1 min 15 cycles

96° C, 10 sec.

70° C, 1 min. 15 cycles

4° C soak

When done cycling, using the Robbins Hydra 290 add 100 µl of 100 % ethanol to the

10 A reaction cycle plate and pool the contents of all four cycle plates into the appropriate well.

To perform ethanol precipitation: Use Hydra program 4 to add 100 µl 100% ethanol to each A tray. Use Hydra program 5 to transfer the ethanol and therefore combine the samples from plate to plate. Once the G, A, T, and C trays of each block
15 are mixed, spin for 30 minutes at 3250 in the Beckman. Pour off the ethanol with a firm shake and blot on a paper towel before drying in the speed vac (~10 minutes or until dry). If ready to load add 3 µl dye and denature in the oven at 95° C for ~5 minutes and load 2 µl. If to store, cover with tape and store at -20°C.

20 Common Solutions

Terrific Broth

Per liter:

900 ml H₂O

12 g bacto tryptone

25 24 g bacto-yeast extract

4 ml glycerol

Shake until dissolved and then autoclave. Allow the solution to cool to 60° C or less and then add 100 ml of sterile 0.17M KH₂PO₄, 0.72M K₂HPO₄ (in the hood w/ sterile
30 technique).

0.17M KH₂PO₄, 0.72M K₂HPO₄

Dissolve 2.31g of KH_2PO_4 and 12.54g of K_2HPO_4 in 90 ml of H_2O .

Adjust volume to 100 ml with H_2O and autoclave.

Sequence loading Dye

20 ml deionized formamide

5 3.6 ml dH_2O

400 μl 0.5M EDTA, pH 8.0

0.2 g Blue Dextran

*Light sensitive, cover in foil or store in the dark.

10 STET/TWEEN

10 ml 5M NaCl

5 ml 1M Tris, pH 8.0

1 ml 0.5M EDTA., pH 8.0

25ml Tween20

15 Bring volume to 500 ml with H_2O

The sequencing reactions are run on an ABI 377 sequencer per manufacturer's instructions. The sequencing information obtained each run are analyzed as follows.

Sequencing reads are screened for ribosomal., mitochondrial., chloroplast or human sequence contamination.. In good sequences, vector is marked by x's. These

20 sequences go into biolims regardless of whether or not they pass the criteria for a 'good' sequence. This criteria is ≥ 100 bases with phred score of ≥ 20 and 15 of these bases adjacent to each other.

Sequencing reads that pass the criteria for good sequences are downloaded for assembly into consensus sequences (contigs). The program Phrap (copyrighted by Phil
25 Green at University of Washington, Seattle, WA) utilizes both the Phred sequence information and the quality calls to assemble the sequencing reads. Parameters used with Phrap were determined empirically to minimize assembly of chimeric sequences and maximize differential detection of closely related members of gene families. The following parameters were used with the Phrap program to perform the assembly:

| | | |
|----------|----|---|
| Penalty | -6 | Penalty for mismatches(substitutions) |
| Minmatch | 40 | Minimum length of matching sequence to use in assembly of |

| | | |
|--------------|----|--|
| | | reads |
| Trim penalty | 0 | penalty used for identifying degenerate sequence at beginning and end of read. |
| Minscore | 80 | Minimum alignment score |

Results from the Phrap analysis yield either contigs consisting of a consensus of two or more overlapping sequence reads, or singlets that are non-overlapping .

The contig and singlets assembly were further analyzed to eliminate low quality sequence utilizing a program to filter sequences based on quality scores generated by the Phred program. The threshold quality for “high quality” base calls is 20. Sequences with less than 50 contiguous high quality bases calls at the beginning of the sequence, and also at the end of the sequence were discarded. Additionally, the maximum allowable percentage of “low quality base calls in the final sequence is 2%, otherwise the sequence is discarded.

The stand-alone BLAST programs and Genbank databases were downloaded from NCBI for use on secure servers at the Paradigm Genetics, Inc. site. The sequences from the assembly were compared to the GenBank NR database downloaded from NCBI using the gapped version (2.0) of BLASTX. BLASTX translates the DNA sequence in all six reading frames and compares it to an amino acid database.

Low complexity sequences are filtered in the query sequence. (Altschul *et al.* (1997) Nucleic Acids Res **25**(17):3389-402).

Genbank sequences found in the BLASTX search with an E Value of less than $1e^{-10}$ are considered to be highly similar, and the Genbank definition lines were used to annotate the query sequences.

When no significantly similar sequences were found as a result of the BLASTX search, the query sequences were compared with the PROSITE database (Bairoch, A. (1992) PROSITE: A dictionary of sites and patterns in proteins. Nucleic Acids Research 20:2013-2018.) to locate functional motifs.

Query sequences were first translated in six reading frames using the Wisconsin GCG pepdata program (Wisconsin Package Version 10.0, Genetics Computer Group (GCG) , Madison, Wisconsin, USA.). The Wisconsin GCG motifs program (Wisconsin Package Version 10.0, Genetics Computer Group (GCG) , Madison, Wisconsin, USA.)

was used to locate motifs in the peptide sequence, with no mismatches allowed. Motif names from the PROSITE results were used to annotate these query sequences.

Table 1

| SEQ ID | Reference | Annotation |
|--------|-----------|--|
| 1 | 2023001 | 0 >emb CAB10331.1 (Z97339) pyruvate, orthophosphate dikinase [Arabidopsis thaliana] Length = 960 |
| 2 | 2023002 | 1E-169 >sp O02654 ENO_LOLPE ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 1911573 bbs 175625 (S80961) enolase [Loligo pealii=squids, nervous system, Peptide, 434 aa] [Loligo pealei] Length = 434 |
| 3 | 2023003 | 0 >gi 1669387 (U41998) actin 2 [Arabidopsis thaliana] Length = 377 |
| 4 | 2023004 | 1E-10 >sp P44677 TOLB_HAEIN TOLB PROTEIN PRECURSOR >gi 1073946 pir F64064 colicin tolerance protein (tolB) homolog - Haemophilus influenzae (strain Rd KW20) >gi 1573352 (U32722) colicin tolerance protein (tolB) [Haemophilus influenzae Rd] Length = 427 |
| 5 | 2023005 | 0 >gi 2062164 (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana] Length = 470 |
| 6 | 2023006 | 0 >emb CAA20523.1 (AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi 4559345 gb AAD23006.1 AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana] Length = 355 |
| 7 | 2023007 | 0 >sp P31167 ADT1_ARATH ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 99658 pir S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi 16175 emb CAA46518 (X65549) adenylate translocator [Arabidopsis thaliana] >gi 445607 prf 1909354A adenylate translocator [Arabidopsis thaliana] Length = 379 |
| 8 | 2023008 | 0 >sp P29517 TBB9_ARATH TUBULIN BETA-9 CHAIN >gi 320190 pir JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi 166910 (M84706) beta-9 tubulin [Arabidopsis thaliana] >gi 5262779 emb CAB45884.1 (AL080282) tubulin beta-9 chain [Arabidopsis thaliana] Length = 444 |
| 9 | 2023009 | 0 >pir S71288 magnesium chelatase chain - Arabidopsis thaliana >gi 1154627 emb CAA92802 (Z68495) magnesium chelatase subunit [Arabidopsis thaliana] Length = 1381 |
| 10 | 2023010 | 1E-133 >sp P92966 RS41_ARATH ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi 1707370 emb CAA67799 (X99436) splicing factor [Arabidopsis thaliana] Length = 356 |
| 11 | 2023011 | 0 >dbj BAA11682 (D83025) proline oxidase precursor [Arabidopsis thaliana] Length = 499 |
| 12 | 2023012 | 0 >sp P17614 ATP2_NICPL ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi 82133 pir A24355 H+-transporting ATP synthase (EC 3.6.1.34) beta-1 chain, mitochondrial - curled-leaved tobacco >gi 19685 emb CAA26620 (X02868) ATP synthase beta subunit [Nicotiana plumbaginifolia] Length = 560 |
| 13 | 2023013 | 0 >gi 2160158 (AC000132) Similar to elongation factor 1-gamma (gb EF1G_XENLA). ESTs gb T20564,gb T45940,gb T04527 come from this gene. [Arabidopsis thaliana] Length = 414 |
| 14 | 2023014 | Rgd(2092-2094) |
| 15 | 2023015 | 0 >sp P49676 BGAL_BRAOL BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi 1076460 pir S52393 beta-galactosidase (EC 3.2.1.23) - wild cabbage >gi 669059 emb CAA59162 (X84684) beta-galactosidase [Brassica oleracea] Length = 828 |
| 16 | 2023016 | 0 >pir S08534 translation elongation factor eEF-1 alpha chain (gene A4) |

| | | |
|----|---------|--|
| | | - Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432) elongation factor 1-alpha [Arabidopsis thaliana] Length = 449 |
| 17 | 2023017 | 2E-68 >gi 4091806 (AF052585) CONSTANS-like protein 2 [Malus domestica] Length = 329 |
| 18 | 2023018 | 0 >sp O24456 GBLP_ARATH GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi 2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana] Length = 327 |
| 19 | 2023019 | 1E-140 >sp Q03460 GLSN_MEDSA GLUTAMATE SYNTHASE [NADH] PRECURSOR (NADH-GOGAT) >gi 484529 pir JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi 166412 (L01660) NADH-glutamate synthase [Medicago sativa] Length = 2194 |
| 20 | 2023020 | 1E-159 >gi 2677828 (U93166) cysteine protease [Prunus armeniaca] Length = 358 |
| 21 | 2023021 | 3E-74 >sp P31167 ADT1_ARATH ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 99658 pir S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi 16175 emb CAA46518 (X65549) adenylate translocator [Arabidopsis thaliana] >gi 445607 prf 1909354A adenylate translocator [Arabidopsis thaliana] Length = 379 |
| 22 | 2023022 | 1E-136 >pir S71265 ferritin - Arabidopsis thaliana >gi 1246401 emb CAA63932 (X94248) ferritin [Arabidopsis thaliana] Length = 255 |
| 23 | 2023023 | 0 >sp P25856 G3PA_ARATH GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi 2117520 pir JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi 166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi 1402885 emb CAA66816 (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana] Length = 396 |
| 24 | 2023024 | Tyr Phospho Site(1382-1388) |
| 25 | 2023025 | 0 >gi 2062167 (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana] Length = 322 |
| 26 | 2023026 | 0 >gi 3834314 (AC005679) Similar to gene pi010 glycosyltransferase gi 2257490 from S. pombe clone 1750 gb AB004534. ESTs gb T46079 and gb AA394466 come from this gene. [Arabidopsis thaliana] Length = 405 |
| 27 | 2023027 | 0 >sp P25856 G3PA_ARATH GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi 2117520 pir JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi 166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi 1402885 emb CAA66816 (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana] Length = 396 |
| 28 | 2023028 | 1E-170 >pir UQMUM ubiquitin precursor - Arabidopsis thaliana >gi 17678 emb CAA31331 (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi 987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi 226499 prf 1515347A poly-ubiquitin [Arabidopsis thaliana] Length = 382 |
| 29 | 2023029 | 3E-71 >sp P37707 B2_DAUCA B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus carota] Length = 207 |
| 30 | 2023030 | 0 >sp P49078 ASNS_ARATH ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 507946 (L29083) glutamine-dependent asparagine synthetase [Arabidopsis thaliana] >gi 5541701 emb CAB51206.1 (AL096860) glutamine-dependent asparagine synthetase [Arabidopsis thaliana] Length = 584 |
| 31 | 2023031 | 2E-25 >gb AAD24193.1 AF134238_1 (AF134238) PL6 protein [Mus musculus] Length = 350 |

| | | |
|----|---------|--|
| 32 | 2023032 | 1E-149 >sp P04778 CB22_ARATH CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana] Length = 267 |
| 33 | 2023033 | 1E-153 >gi 1915974 (U62329) fructokinase [Lycopersicon esculentum] >gi 2102693 (U64818) fructokinase [Lycopersicon esculentum] Length = 328 |
| 34 | 2023034 | 1E-106 >sp Q64516 GLPK_MOUSE GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) >gi 1480469 (U48403) glycerol kinase [Mus musculus] Length = 524 |
| 35 | 2023035 | 1E-103 >emb CAA16745.1 (AL021711) heat shock transcription factor-like protein [Arabidopsis thaliana] Length = 401 |
| 36 | 2023036 | 1E-170 >gi 2286153 (AF007581) cytoplasmic malate dehydrogenase [Zea mays] Length = 332 |
| 37 | 2023037 | Tyr_Phospho_Site(1338-1344) |
| 38 | 2023038 | 1E-179 >sp P19456 PMA2_ARATH PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi 166629 (J05570) H+-ATPase [Arabidopsis thaliana] >gi 5730129 emb CAB52463.1 (AL109796) H+-transporting ATPase type 2, plasma membrane [Arabidopsis thaliana] Length = 948 |
| 39 | 2023039 | Pkc_Phospho_Site(5-7) |
| 40 | 2023040 | Tyr_Phospho_Site(830-837) |
| 41 | 2023041 | 8E-98 >gi 4204274 (AC004146) ribulose biphosphate carboxylase, small subunit [Arabidopsis thaliana] Length = 180 |
| 42 | 2023042 | 1E-175 >emb CAB38206 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana] Length = 603 |
| 43 | 2023043 | Pkc_Phospho_Site(19-21) |
| 44 | 2023044 | 9E-58 >sp P26599 PTB_HUMAN POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1) >gi 35768 emb CAA43973 (X62006) polypirimidine tract binding protein [Homo sapiens] >gi 35774 emb CAA43056 (X60648) polypyrimidine tract-binding protein (pPTB) [Homo sapiens] >gi 4096061 (AC006273) PTB_HUMAN; PTB; HETEROGENEOUS NUCLEA; HNRNP I; 57 KD RNA-BINDING PROTEIN PPTB-1 [Homo sapiens] Length = 531 |
| 45 | 2023045 | 2E-79 >gi 2642429 (AC002391) poly(A)-binding protein [Arabidopsis thaliana] Length = 662 |
| 46 | 2023046 | 0 >sp Q38854 CLA1_ARATH PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE PRECURSOR (DXP SYNTHASE) >gi 1399261 (U27099) DEF [Arabidopsis thaliana] Length = 717 |
| 47 | 2023047 | Wd_Repeats(1245-1259) |
| 48 | 2023048 | 1E-151 >dbj BAA25181 (D88537) delta 9 desaturase [Arabidopsis thaliana] Length = 307 |
| 49 | 2023049 | 1E-167 >emb CAB43488.1 (AJ012278) ATP-dependent Clp protease subunit ClpP [Arabidopsis thaliana] >gi 5360579 dbj BAA82065.1 (AB022326) nClpP1 [Arabidopsis thaliana] Length = 298 |
| 50 | 2023050 | 0 >emb CAA67339 (X98807) peroxidase ATP21a [Arabidopsis thaliana] Length = 329 |
| 51 | 2023051 | 0 >gb AAD39650.1 AC007591_15 (AC007591) Similar to gb Z70524 PDR5-like ABC transporter from Spirodela polyrrhiza and is a member of the PF 00005 ABC transporter family. ESTs gb N97039 and gb T43169 come from this gene. [Arabid |
| 52 | 2023052 | 5E-52 >sp P41227 ARDH_HUMAN N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi 517485 emb CAA54691 (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi 1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens] Length = 235 |
| 53 | 2023053 | 1E-126 >gi 3158476 (AF067185) aquaporin 2 [Samanea saman] Length |

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| | | = 287 |
| 54 | 2023054 | 1E-173 >gi 3212877 (AC004005) Lea-like protein [Arabidopsis thaliana] Length = 325 |
| 55 | 2023055 | 1E-14 >sp Q28955 PNAD_PIG PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) >gi 1082956 pir A55768 asparaginyl-peptide amidohydrolase (EC 3.5.1.-) - pig >gi 595950 (U17062) protein N-terminal asparagine amidohydrolase [Sus scrofa] Length = 310 |
| 56 | 2023056 | 1E-172 >sp P53799 FDFT_ARATH FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi 1076324 pir S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi 798820 emb CAA60385 (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi 806325 dbj BAA06103 (D29017) squalene synthase [Arabidopsis thaliana] >gi 2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi 3096933 emb CAA18843.1 (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi 4098519 (U79159) squalene synthase [Arabidopsis thaliana] Length = 410 |
| 57 | 2023057 | 1E-141 >gi 3413700 (AC004747) YME1 protein [Arabidopsis thaliana] Length = 627 |
| 58 | 2023058 | Tyr_Phospho_Site(1667-1673) |
| 59 | 2023059 | 1E-144 >sp Q08682 RSP4_ARATH 40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG) >gi 322536 pir S30570 laminin receptor homolog - Arabidopsis thaliana >gi 16380 emb CAA48794 (X69056) laminin receptor homologue [Arabidopsis thaliana] Length = 298 |
| 60 | 2023060 | 2E-43 >gi 2735550 (U96638) unc-50 related protein; URP [Rattus norvegicus] Length = 259 |
| 61 | 2023061 | Tyr_Phospho_Site(65-73) |
| 62 | 2023062 | 2E-30 >emb CAB03470.1 (Z81137) Similarity to Yeast YIP1 protein (SW:P53039); cDNA EST EMBL:T01608 comes from this gene; cDNA EST EMBL:C07393 comes from this gene; cDNA EST EMBL:C07550 comes from this gene; cDNA EST EMBL:C08746 comes from this gene... Length = 282 |
| 63 | 2023063 | 1E-151 >gi 1773330 (U80071) glycolate oxidase [Mesembryanthemum crystallinum] Length = 370 |
| 64 | 2023064 | 7E-44 >ref NP_006339.1 PGTC90 Golgi transport complex protein (90 kDa) >gi 3808235 (AF058718) 13 S Golgi transport complex 90kD subunit brain-specific isoform [Homo sapiens] Length = 839 |
| 65 | 2023065 | 1E-168 >emb CAB44681.1 (AL078620) mitochondrial carrier-like protein [Arabidopsis thaliana] Length = 330 |
| 66 | 2023066 | 4E-12 >gi 1764100 (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis thaliana] Length = 373 |
| 67 | 2023067 | 2E-22 >gb AAD48936.1 AF160760_4 (AF160760) contains similarity to Pfam family PF0040 - WD domain, G-beta repeat; score=10.8, E=3.2, N=2 [Arabidopsis thaliana] Length = 892 |
| 68 | 2023068 | 1E-123 >sp P30302 WC2C_ARATH PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN) (WSI-TIP) >gi 217869 dbj BAA02520 (D13254) transmembrane channel protein [Arabidopsis thaliana] >gi 4371283 gb AAD18141 (AC006260) plasma membrane intrinsic protein 2C [Arabidopsis thaliana] >gi 384324 prf 1905411A transmembrane channel [Arabidopsis thaliana] Length = 285 |
| 69 | 2023069 | 6E-12 >dbj BAA74463 (AB022605) mRNA (guanine-7-)methyltransferase [Homo sapiens] Length = 504 |
| 70 | 2023070 | 1E-153 >gi 2062161 (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana] Length = 298 |
| 71 | 2023071 | 1E-157 >sp P43286 WC2A_ARATH PLASMA MEMBRANE INTRINSIC |

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| | | PROTEIN 2A >gi 629542 pir S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi 472877 emb CAA53477 (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana] Length = 287 |
| 72 | 2023072 | 9E-98 >gi 2252840 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi 6049882 gb AAF02797.1 AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] Length = 746 |
| 73 | 2023073 | 9E-97 >gb AAF00673.1 AC008153_25 (AC008153) 2-cys peroxiredoxin BAS1 precursor (thiol-specific antioxidant protein) [Arabidopsis thaliana] >gi 6041816 gb AAF02131.1 AC009918_3 (AC009918) 2-cys peroxiredoxin [Arabidopsis thaliana] Length = 301 |
| 74 | 2023074 | 1E-168 >emb CAA06460 (AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi 3093276 emb CAA06671.1 (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi 4191787 (AC005917) cytidine deaminase [Arabidopsis thaliana] >gi 6090835 gb AAF03358.1 AF134487_1 (AF134487) cytidine deaminase 1 [Arabidopsis thaliana] Length = 301 |
| 75 | 2023075 | 0 >emb CAA66863 (X98190) peroxidase ATP2a [Arabidopsis thaliana] >gi 4371288 gb AAD18146 (AC006260) peroxidase ATP2a [Arabidopsis thaliana] Length = 327 |
| 76 | 2023076 | 1E-159 >sp Q08733 WC1C_ARATH PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi 396218 emb CAA49155 (X69294) transmembrane protein TMP-B [Arabidopsis thaliana] Length = 286 |
| 77 | 2023077 | Rgd(840-842) |
| 78 | 2023078 | 1E-157 >emb CAB10405.1 (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana] Length = 306 |
| 79 | 2023079 | 1E-110 >gi 3341679 (AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana] Length = 613 |
| 80 | 2023080 | 1E-79 >gb AAA02747.1 (L13655) membrane protein [Saccharum hybrid cultivar H65-7052] Length = 325 |
| 81 | 2023081 | 1E-155 >pir S33443 chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis thaliana] Length = 290 |
| 82 | 2023082 | 0 >emb CAB56580.1 (AJ011628) squamosa promoter binding protein-like 1 [Arabidopsis thaliana] Length = 881 |
| 83 | 2023083 | Tyr_Phospho_Site(305-312) |
| 84 | 2023084 | 6E-22 >gb AAD46141.1 AF081022_1 (AF081022) hypoxia-induced protein kinase L31 [Lycopersicon esculentum] Length = 78 |
| 85 | 2023085 | 1E-154 >gi 2281109 (AC002333) endochitinase isolog [Arabidopsis thaliana] Length = 281 |
| 86 | 2023086 | 1E-79 >gi 3415117 (AF081203) villin 3 [Arabidopsis thaliana] Length = 966 |
| 87 | 2023087 | 1E-103 >ref NP_005435.1 PRCD1+ protein involved in sexual development >gi 1620898 dbj BAA13508 (D87957) protein involved in sexual development [Homo sapiens] Length = 299 |
| 88 | 2023088 | 1E-106 >sp Q05047 CP72_CATRO CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi 167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi 445604 prf 1909351A cytochrome P450 [Catharanthus roseus] Length = 524 |
| 89 | 2023089 | 5E-41 >ref NP_000511.1 PHEXA hexosaminidase A (alpha polypeptide) >gi 123079 sp P06865 HEXA_HUMAN BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (N-ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) >gi 67503 pir AOHUBA beta-N-acetylhexosaminidase (EC 3.2.1.52) alpha chain precursor - human >gi 179458 (M16424) beta-hexosaminidase alpha chain [Homo sapiens] >gi 4261632 gb AAD13932 1680052_1 (S62076) lysosomal enzyme beta-N- |

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| | | acetylhexosaminidase A [Homo sapiens] Length = 529 |
| 90 | 2023090 | 0 >emb CAB36796.1 (AL035525) pectinesterase-like protein [Arabidopsis thaliana] Length = 477 |
| 91 | 2023091 | 1E-139 >emb CAB10240.1 (Z97336) disease resistance RPS2 like protein [Arabidopsis thaliana] Length = 719 |
| 92 | 2023092 | 1E-170) >pir S49332 seed tetraubiquitin - common sunflower >gi 303901 dbj BAA03764 (D16248) ubiquitin [Glycine max] >gi 456714 dbj BAA05670 (D28123) Ubiquitin [Glycine max] >gi 556688 emb CAA84440 (Z34988) seed tetraubiquitin [Helianthus annuus] >gi 994785 dbj BAA05085 (D26092) Ubiquitin [Glycine max] >gi 4263514 gb AAD15340 (AC004044) polyubiquitin [Arabidopsis thaliana] >gi 1096513 prf 2111434A tetraubiquitin [Helianthus annuus] Length = 305 |
| 93 | 2023093 | 1E-146 >gi 2088652 (AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi 2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana] Length = 293 |
| 94 | 2023094 | 0 >pir B45511 chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis thaliana >gi 166666 (M38240) basic chitinase [Arabidopsis thaliana] >gi 5689104 dbj BAA82811.1 (AB023449) basic endochitinase [Arabidopsis thaliana] >gi 5689106 dbj BAA82812.1 (AB023450) basic endochitinase [Arabidopsis thaliana] >gi 5689108 dbj BAA82813.1 (AB023451) basic endochitinase [Arabidopsis thaliana] >gi 5689112 dbj BAA82815.1 (AB023453) basic endochitinase [Arabidopsis thaliana] >gi 5689114 dbj BAA82816.1 (AB023454) basic endochitinase [Arabidopsis thaliana] >gi 5689120 dbj BAA82819.1 (AB023457) basic endochitinase [Arabidopsis thaliana] >gi 5689122 dbj BAA82820.1 (AB023458) basic endochitinase [Arabidopsis thaliana] >gi 5689124 dbj BAA82821.1 (AB023459) basic endochitinase [Arabidopsis thaliana] >gi 5689126 dbj BAA82822.1 (AB023460) basic endochitinase [Arabidopsis thaliana] >gi 5689128 dbj BAA82823.1 (AB023461) basic endochitinase [Arabidopsis thaliana] >gi 5689132 dbj BAA82825.1 (AB023463) basic endochitinase [Arabidopsis thaliana] Length = 335 |
| 95 | 2023095 | Tyr_Phospho_Site(1027-1033) |
| 96 | 2023096 | 1E-152 >pir S23546 chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] Length = 265 |
| 97 | 2023097 | Tyr_Phospho_Site(98-104) |
| 98 | 2023098 | 1E-133 >emb CAB38813.1 (AL035679) ubiquitin-dependent proteolytic protein [Arabidopsis thaliana] Length = 315 |
| 99 | 2023099 | 5E-45 >gb AAD26911.1 AC006429_1 (AC006429) auxin down-regulated protein [Arabidopsis thaliana] Length = 291 |
| 100 | 2023100 | 1E-169 >sp P46523 CLPA_BRANA ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA PRECURSOR >gi 480969 pir S37557 clpA protein - rape (fragment) >gi 406311 emb CAA53077 (X75328) clpA [Brassica napus] Length = 874 |
| 101 | 2023101 | 1E-100 >gb AAD28780.1 AF134133_1 (AF134133) Lil3 protein [Arabidopsis thaliana] Length = 262 |
| 102 | 2023102 | 4E-42 >gi 3329368 (AF031244) nodulin-like protein [Arabidopsis thaliana] Length = 559 |
| 103 | 2023103 | Tyr_Phospho_Site(206-212) |
| 104 | 2023104 | Tyr_Phospho_Site(740-748) |
| 105 | 2023105 | 1E-130 >pir S20866 L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment) Length = 263 |
| 106 | 2023106 | 2E-15 >gi 4093153 (AF088280) phytochrome-associated protein 3 |

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| | | [Arabidopsis thaliana] Length = 524 |
| 107 | 2023107 | Zinc_Protease(1292-1301) |
| 108 | 2023108 | 1E-148 >dbj BAA32735 (AB011545) GF14 mu [Arabidopsis thaliana] >gi 4559343 gb AAD23005.1 AC007087_24 (AC007087) DNA regulatory protein GF14 mu [Arabidopsis thaliana] >gi 5802796 gb AAD51784.1 AF145301_1 (AF145301) 14-3-3 protein GF14 mu [Arabidopsis thaliana] Length = 263 |
| 109 | 2023109 | Zinc_Finger_C3hc4(138-147) |
| 110 | 2023110 | 2E-49 >dbj BAA16833 (D90901) spore germination protein c2 [Synechocystis sp.] Length = 238 |
| 111 | 2023111 | 2E-44 >emb CAA21916.1 (AL033389) yeast cell division cycle CDC50 homolog [Schizosaccharomyces pombe] Length = 396 |
| 112 | 2023112 | Zinc_Finger_C2h2(879-903) |
| 113 | 2023113 | 3E-66 >gb AAD39835.1 AF057024_1 (AF057024) Ran-binding protein siRanBP [Arabidopsis thaliana] Length = 234 |
| 114 | 2023114 | 1E-173 >gb AAD38248.1 AC006193_4 (AC006193) membrane related protein [Arabidopsis thaliana] Length = 385 |
| 115 | 2023115 | Tyr_Phospho_Site(1708-1714) |
| 116 | 2023116 | 5E-63 >emb CAA69300 (Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi 2982443 emb CAA18251.1 (AL022224) endomembrane-associated protein [Arabidopsis thaliana] Length = 225 |
| 117 | 2023117 | 2E-46 >gi 451193 (L28008) wali7 [Triticum aestivum] >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum] Length = 270 |
| 118 | 2023118 | 1E-102 >pir S58499 IAA13 protein - Arabidopsis thaliana >gi 972929 (U18415) IAA13 [Arabidopsis thaliana] >gi 2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana] Length = 246 |
| 119 | 2023119 | Tyr_Phospho_Site(14-21) |
| 120 | 2023120 | 1E-147 >sp P27521 CB24_ARATH CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR (LHCI TYPE III CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana] Length = 251 |
| 121 | 2023121 | Tyr_Phospho_Site(414-421) |
| 122 | 2023122 | 3E-59 >emb CAB10557.1 (Z97344) trehalose-6-phosphate synthase like protein [Arabidopsis thaliana] Length = 865 |
| 123 | 2023123 | Tyr_Phospho_Site(110-117) |
| 124 | 2023124 | 1E-109 >dbj BAA33810.1 (AB018441) phi-1 [Nicotiana tabacum] Length = 313 |
| 125 | 2023125 | 1E-120 >emb CAB56038.1 (AJ011049) tyrosine decarboxylase [Arabidopsis thaliana] Length = 489 |
| 126 | 2023126 | Tyr_Phospho_Site(640-647) |
| 127 | 2023127 | 3E-44 >ref NP_005818.1 PUGTREL1 UDP-galactose transporter related >gi 2136346 pir JC5024 UDP-galactose transporter related isozyme 1 - human >gi 1669560 dbj BAA13525.1 (D87989) UGTrel1 [Homo sapiens] Length = 322 |
| 128 | 2023128 | 1E-115 >sp P42055 POR4_SOLTU 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) >gi 629720 pir S46936 34K porin - potato >gi 1076682 pir A55364 porin (clone pPOM-34) - potato mitochondrion >gi 516166 emb CAA56599 (X80386) 34 kDa porin [Solanum tuberosum] Length = 276 |
| 129 | 2023129 | Tyr_Phospho_Site(25-32) |
| 130 | 2023130 | 1E-76 >sp Q42656 AGAL_COFA ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi 504489 (L27992) alpha-galactosidase [Coffea arabica] Length = 378 |
| 131 | 2023131 | 2E-20 >gb AAF01440.1 AF187961_1 (AF187961) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe] Length = 1129 |
| 132 | 2023132 | 1E-141 >emb CAA17567 (AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana] Length = 259 |

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| 133 | 2023133 | 1E-97 >emb CAA64565 (X95269) LRR protein [Lycopersicon esculentum] Length = 221 |
| 134 | 2023134 | 3E-53 >dbj BAA24576 (AB000778) phospholipase D [Rattus norvegicus] Length = 1074 |
| 135 | 2023135 | 9E-48 >sp P27061 PPA1_LYCES ACID PHOSPHATASE PRECURSOR 1 >gi 170370 (M83211) acid phosphatase type 1 [Lycopersicon esculentum] >gi 170372 (M67474) acid phosphatase type 5 [Lycopersicon esculentum] >gi 445121 prf 1908427A acid phosphatase 1 [Lycopersicon esculentum] Length = 255 |
| 136 | 2023136 | 1E-138 >gi 3421072 (AF043519) 20S proteasome subunit PAA2 [Arabidopsis thaliana] >gi 4006819 gb AAC95161.1 (AC005970) 20S proteasome subunit PAA2 [Arabidopsis thaliana] Length = 246 |
| 137 | 2023137 | 2E-75 >gb AAD14602 (AF092910) stage specific peptide 24 [Trypanosoma cruzi] Length = 287 |
| 138 | 2023138 | 1E-158 >pir S59519 tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi 619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi 1585768 prf 2201482A Trp synthase:SUBUNIT=alpha [Arabidopsis thaliana] Length = 312 |
| 139 | 2023139 | Tyr Phospho Site(892-900) |
| 140 | 2023140 | 3E-53 >emb CAB43522.1 (AJ238804) non-specific lipid transfer protein [Arabidopsis thaliana] Length = 118 |
| 141 | 2023141 | 1E-165 >pir S71226 xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] Length = 289 |
| 142 | 2023142 | 1E-146 >gb AAD55272.1 AC008263_3 (AC008263) Identical to gb AF078080 isochorismate synthase from Arabidopsis thaliana. ESTs gb R90272, gb A1100274 and gb T42189 come from this gene. Length = 503 |
| 143 | 2023143 | 1E-158 >sp P43285 WC1A_ARATH PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi 629540 pir S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi 472873 emb CAA53475 (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana] Length = 286 |
| 144 | 2023144 | 1E-173 >sp Q38882 PLD_ARATH PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi 1297302 (U36381) phospholipase D [Arabidopsis thaliana] Length = 809 |
| 145 | 2023145 | 3E-97 >sp Q03943 IM30_PEA CHLOROPLAST MEMBRANE-ASSOCIATED 30 KD PROTEIN PRECURSOR (M30) >gi 1076532 pir S47966 probable lipid transfer protein M30 precursor - garden pea >gi 169107 (M73744) IM30 [Pisum sativum] Length = 323 |
| 146 | 2023146 | 1E-167 >sp P55737 HS82_ARATH HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B heat shock protein HSP81-2 [Arabidopsis thaliana] Length = 699 |
| 147 | 2023147 | Pkc Phospho Site(56-58) |
| 148 | 2023148 | 3E-26 >dbj BAA75919.1 (AB009340) tartrate-resistant acid phosphatase [Oryctolagus cuniculus] Length = 325 |
| 149 | 2023149 | 1E-159 >emb CAA17774.1 (AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana] Length = 280 |
| 150 | 2023150 | 1E-155 >gi 2443883 (AC002294) Similar to RPS-2 disease resistance protein [Arabidopsis thaliana] Length = 967 |
| 151 | 2023151 | 1E-99 >gb AAD29800.1 AC006264_8 (AC006264) signal sequence receptor, alpha subunit (SSR-alpha) [Arabidopsis thaliana] Length = 257 |
| 152 | 2023152 | Tyr Phospho Site(642-650) |
| 153 | 2023153 | 2E-64 >gb AAC78271.1 AAC78271 (AC002330) glutamate-/aspartate-binding peptide [Arabidopsis thaliana] Length = 248 |
| 154 | 2023154 | 1E-172 >gi 4218963 (AF093672) xyloglucan endotransglycosylase |

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| | | [Arabidopsis thaliana] >gi 4539300 emb CAB39603.1 (AL049480) xyloglucan endo-1, 4-beta-D-glucanase [Arabidopsis thaliana] Length = 287 |
| 155 | 2023155 | Zinc_Finger_C2h2(917-941) |
| 156 | 2023156 | 1E-108 >emb CAA65416 (X96598) CaLB protein [Arabidopsis thaliana] Length = 493 |
| 157 | 2023157 | 5E-26 >emb CAA64425 (X94976) cell wall-plasma membrane linker protein [Brassica napus] Length = 376 |
| 158 | 2023158 | 1E-159 >gb AAD25750.1 AC007060_8 (AC007060) Strong similarity to F19I3.7 gi 3033380 coatomer epsilon subunit from Arabidopsis thaliana BAC gb AC004238. ESTs gb Z17908, gb AA728673, gb N96555, gb H76335, gb AA712463, gb W43247, gb T45611, g... Length = 292 |
| 159 | 2023159 | Tyr_Phospho_Site(958-964) |
| 160 | 2023160 | 5E-14 >emb CAA18475.1 (AL022347) serine /threonine kinase-like protein, receptor kinase [Arabidopsis thaliana] Length = 656 |
| 161 | 2023161 | 3E-33 >sp P26568 H11_ARATH HISTONE H1.1 >gi 1070594 pir HSMU11 histone H1.1 - Arabidopsis thaliana >gi 16317 emb CAA44314 (X62458) Histone H1 [Arabidopsis thaliana] Length = 274 |
| 162 | 2023162 | 2E-97 >emb CAA07573.1 (AJ007586) src2-like protein [Arabidopsis thaliana] Length = 324 |
| 163 | 2023163 | Tyr_Phospho_Site(246-254) |
| 164 | 2023164 | 1E-171 >sp Q42547 CAT3_ARATH CATALASE 3 >gi 2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi 2511726 (AF021937) catalase 3 [Arabidopsis thaliana] Length = 492 |
| 165 | 2023165 | Tyr_Phospho_Site(75-83) |
| 166 | 2023166 | 1E-151 >emb CAA66966 (X98322) peroxidase [Arabidopsis thaliana] >gi 1429219 emb CAA67312 (X98776) peroxidase ATP13a [Arabidopsis thaliana] Length = 313 |
| 167 | 2023167 | 7E-38 >emb CAB41106.1 (AL049656) myb-like protein [Arabidopsis thaliana] Length = 261 |
| 168 | 2023168 | 8E-74 >gi 4008006 (AF084034) receptor-like protein kinase [Arabidopsis thaliana] Length = 645 |
| 169 | 2023169 | 1E-137 >pir JQ1678 transcription factor tga1 - Arabidopsis thaliana >gi 16550 emb CAA48189 (X68053) transcription factor [Arabidopsis thaliana] Length = 367 |
| 170 | 2023170 | 8E-57 >gi 3184559 (AF052290) c-type cytochrome biogenesis protein [Synechococcus PCC7002] Length = 246 |
| 171 | 2023171 | 1E-103 >gb AAD32768.1 AC007661_5 (AC007661) alpha-carboxyltransferase [Arabidopsis thaliana] Length = 796 |
| 172 | 2023172 | 1E-117 >gb AAD32822.1 AC007659_4 (AC007659) phosphatidate cytidyltransferase [Arabidopsis thaliana] Length = 430 |
| 173 | 2023173 | 1E-129 >dbj BAA32210 (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana] Length = 770 |
| 174 | 2023174 | 2E-76 >gi 3157927 (AC002131) Contains similarity to GDP-dissociation inhibitor gb L07918 from Mus musculus. [Arabidopsis thaliana] Length = 223 |
| 175 | 2023175 | 2E-89 >pir S68589 serine/threonine-specific kinase (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi 1405837 emb CAA62824 (X91630) receptor-like kinase [Arabidopsis thaliana] >gi 2150023 (AF001168) receptor-like kinase LECRK1 [Arabidopsis thaliana] Length = 661 |
| 176 | 2023176 | 7E-86 >gi 3769673 (AF095285) Tic20 [Pisum sativum] Length = 253 |
| 177 | 2023177 | 2E-17 >sp P46689 GAS1_ARATH GIBBERELLIN-REGULATED PROTEIN 1 PRECURSOR >gi 2129588 pir S71441 GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana >gi 887939 (U11766) GAST1 protein homolog [Arabidopsis thaliana] Length = 98 |
| 178 | 2023178 | 1E-166 >sp O48661 SPEE_ARATH SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY) |

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| | | >gi 2821961 dbj BAA24536 (AB006693) spermidine synthase [Arabidopsis thaliana] Length = 293 |
| 179 | 2023179 | Ww Domain 1(1284-1310) |
| 180 | 2023180 | 1E-104 >pir S27762 Sip1 protein - barley >gi 167100 (M77475) seed imbibition protein [Hordeum vulgare] Length = 757 |
| 181 | 2023181 | 1E-155 >sp P48641 GSHR_ARATH GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (OBP29) >gi 1022797 (U37697) glutathione reductase [Arabidopsis thaliana] Length = 499 |
| 182 | 2023182 | Tyr_Phospho_Site(599-607) |
| 183 | 2023183 | 1E-133 >gi 3688799 (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana] Length = 253 |
| 184 | 2023184 | 1E-110 >gi 3075392 (AC004484) steroid dehydrogenase [Arabidopsis thaliana] Length = 390 |
| 185 | 2023185 | Tyr_Phospho_Site(48-56) |
| 186 | 2023186 | 6E-38 >emb CAA16875.1 (AL021749) receptor protein kinase like protein [Arabidopsis thaliana] Length = 649 |
| 187 | 2023187 | Tyr_Phospho_Site(1737-1743) |
| 188 | 2023188 | 1E-128 >sp P48349 143L_ARATH 14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi 1084332 pir S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi 953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14 lambda [Arabidopsis thaliana] >gi 5802790 gb AAD51781.1 AF145298_1 (AF145298) 14-3-3 protein GF14 lambda [Arabidopsis thaliana] Length = 248 |
| 189 | 2023189 | 1E-135 >emb CAB39932.1 (AL049500) phosphoribosylanthranilate transferase [Arabidopsis thaliana] Length = 857 |
| 190 | 2023190 | Serpin(1794-1804) |
| 191 | 2023191 | 3E-77 >gi 3319340 (AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana] Length = 197 |
| 192 | 2023192 | 1E-47 >emb CAA23033.1 (AL035394) major latex protein [Arabidopsis thaliana] Length = 151 |
| 193 | 2023193 | 7E-76 >gb AAB17191.1 (U73103) laccase [Liriodendron tulipifera] Length = 570 |
| 194 | 2023194 | Tyr_Phospho_Site(712-718) |
| 195 | 2023195 | 1E-161 >sp Q06611 WC1B_ARATH PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi 296085 emb CAA48356 (X68293) transmembrane protein [Arabidopsis thaliana] >gi 3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana] Length = 286 |
| 196 | 2023196 | 1E-16 >sp P44445 RLUD_HAEIN RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE D (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) >gi 1074296 pir F64144 hypothetical protein HI0176 - Haemophilus influenzae (strain Rd KW20) >gi 1573131 (U32702) sfhB protein (sfhB) [Haemophilus influenzae Rd] Length = 324 |
| 197 | 2023197 | 2E-22 >gb AAD48964.1 AF147263_6 (AF147263) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana] Length = 246 |
| 198 | 2023198 | Tyr_Phospho_Site(1422-1428) |
| 199 | 2023199 | Tyr_Phospho_Site(1517-1524) |
| 200 | 2023200 | 1E-109 >gi 2642432 (AC002391) elicitor response element binding protein (WRKY3) [Arabidopsis thaliana] Length = 317 |
| 201 | 2023201 | Tyr_Phospho_Site(271-279) |
| 202 | 2023202 | 1E-176 >gi 3599968 (AF032123) clp protease [Arabidopsis thaliana] Length = 310 |
| 203 | 2023203 | Tyr_Phospho_Site(964-971) |
| 204 | 2023204 | 1E-127 >emb CAA04386 (AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus] Length = 725 |

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| 205 | 2023205 | 4E-32 >emb CAA04124 (AJ000486) methionine gamma-lyase [Trichomonas vaginalis] Length = 396 |
| 206 | 2023206 | 5E-61 >pir S66770 probable membrane protein YOL077c - yeast (Saccharomyces cerevisiae) >gi 1419909 emb CAA99087 (Z74819) ORF YOL077c [Saccharomyces cerevisiae] Length = 291 |
| 207 | 2023207 | 1E-127 >emb CAA66785 (X98108) 23 kDa polypeptide of oxygen-evolving complex (OEC) [Arabidopsis thaliana] Length = 263 |
| 208 | 2023208 | 1E-131 >gb AAF00659.1 AC008153_11 (AC008153) cell division related protein [Arabidopsis thaliana] Length = 663 |
| 209 | 2023209 | 1E-141 >sp P11574 VATB_ARATH VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi 81637 pir A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi 166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana] Length = 492 |
| 210 | 2023210 | 3E-45 >gi 3242706 (AC003040) cyclin-dependent kinase inhibitor protein [Arabidopsis thaliana] >gi 3550262 (AF079587) cyclin-dependent kinase inhibitor; ICK1 [Arabidopsis thaliana] Length = 191 |
| 211 | 2023211 | 1E-140 >gb AAD28777.1 AF134130_1 (AF134130) Lhcb6 protein [Arabidopsis thaliana] Length = 258 |
| 212 | 2023212 | 1E-151) >sp P29511 TBA6_ARATH TUBULIN ALPHA-6 CHAIN >gi 282852 pir JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi 166920 (M84699) TUA6 [Arabidopsis thaliana] >gi 2244853 emb CAB10275.1 (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana] Length = 450 |
| 213 | 2023213 | Tyr_Phospho_Site(405-412) |
| 214 | 2023214 | 1E-175) >emb CAB16823.1 (Z99708) aminopeptidase-like protein [Arabidopsis thaliana] Length = 634 |
| 215 | 2023215 | 2E-33 >emb CAB13047 (Z99110) yjcl [Bacillus subtilis] Length = 396 |
| 216 | 2023216 | 1E-143 >sp Q05466 HAT4_ARATH HOMEBOX-LEUCINE ZIPPER PROTEIN HAT4 (HD-ZIP PROTEIN 4) (HD-ZIP PROTEIN ATHB-2) >gi 629516 pir S31424 homeotic protein Athb-2 - Arabidopsis thaliana >gi 16180 emb CAA48246 (X68145) Athb-2 [Arabido |
| 217 | 2023217 | 1E-149 >emb CAA72487 (Y11791) peroxidase ATP26a [Arabidopsis thaliana] Length = 276 |
| 218 | 2023218 | Tyr_Phospho_Site(404-411) |
| 219 | 2023219 | 1E-138 >gi 2262167 (AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana] Length = 261 |
| 220 | 2023220 | 1E-163 >gb AAD30579.1 AC007260_10 (AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana] Length = 669 |
| 221 | 2023221 | 0) >pir S52150 serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi 2146776 pir S67482 serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi 608577 (L34076) serine acetyltransferase [Arabidopsis thaliana] >gi 608677 emb CAA84371 (Z348 |
| 222 | 2023222 | 1E-116 >emb CAB42903.1 (AL049862) UTP-glucose glucosyltransferase like protein [Arabidopsis thaliana] Length = 478 |
| 223 | 2023223 | 1E-46 >emb CAB10538.2 (Z97343) TEGT protein homolog [Arabidopsis thaliana] Length = 262 |
| 224 | 2023224 | Tyr_Phospho_Site(1002-1010) |
| 225 | 2023225 | 1E-117 >gi 2583121 (AC002387) phosphotransferase [Arabidopsis thaliana] Length = 257 |
| 226 | 2023226 | Tyr_Phospho_Site(732-738) |
| 227 | 2023227 | Tyr_Phospho_Site(1093-1100) |
| 228 | 2023228 | 3E-24 >gb AAD23651.1 AC007119_17 (AC007119) glycine-rich RNA binding protein Ccr2 [Arabidopsis thaliana] Length = 179 |
| 229 | 2023229 | 1E-145 >dbj BAA34250 (AB013886) RAV1 [Arabidopsis thaliana] Length = 344 |

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| 230 | 2023230 | 1E-142 >emb CAB43855.1 (AL078465) isp4 like protein [Arabidopsis thaliana] Length = 753 |
| 231 | 2023231 | 4E-89 >gi 2252866 (AF013294) contains region of similarity to SYT [Arabidopsis thaliana] Length = 230 |
| 232 | 2023232 | 3E-27 >dbj BAA83740.1 (AB023288) TRAB1 [Oryza sativa] Length = 318 |
| 233 | 2023233 | Tyr_Phospho_Site(919-926) |
| 234 | 2023234 | Tyr_Phospho_Site(1189-1196) |
| 235 | 2023235 | Tyr_Phospho_Site(301-307) |
| 236 | 2023236 | 1E-168 >gb AAD56290.1 AF162279_1 (AF162279) 10-formyltetrahydrofolate synthetase [Arabidopsis thaliana] Length = 634 |
| 237 | 2023237 | 1E-112 >gi 3738320 (AC005170) cinnamoyl CoA reductase [Arabidopsis thaliana] Length = 303 |
| 238 | 2023238 | 1E-18 >emb CAA23041.1 (AL035394) Ap2 domain protein [Arabidopsis thaliana] Length = 343 |
| 239 | 2023239 | Tyr_Phospho_Site(393-401) |
| 240 | 2023240 | 4E-22 >gi 699154 (U15180) P450 cytochrome, isopentenyltransf, ferriodox. [Mycobacterium leprae] Length = 187 |
| 241 | 2023241 | 1E-131 >sp P24636 TBB4_ARATH TUBULIN BETA-4 CHAIN >gi 2129546 pir S68122 beta-tubulin 4 - Arabidopsis thaliana >gi 166640 (M21415) beta-tubulin [Arabidopsis thaliana] Length = 444 |
| 242 | 2023242 | 1E-112) >gi 3790581 (AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana] Length = 190 |
| 243 | 2023243 | 1E-124 >emb CAA55006 (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus] Length = 406 |
| 244 | 2023244 | 7E-11 >gi 2622337 (AE000890) inosine-5'-monophosphate dehydrogenase related protein V [Methanobacterium thermoautotrophicum] Length = 187 |
| 245 | 2023245 | 3E-11 >emb CAB45565.1 (AL079355) phospholipase C [Streptomyces coelicolor] Length = 501 |
| 246 | 2023246 | Tyr_Phospho_Site(1121-1127) |
| 247 | 2023247 | 1E-148 >pir S25677 chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi 16366 emb CAA45789 (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128229 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337372 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] Length = 266 |
| 248 | 2023248 | 1E-113 >gi 3941466 (AF062887) transcription factor [Arabidopsis thaliana] Length = 352 |
| 249 | 2023249 | 3E-18 >gb AAD42398.1 AF157493_6 (AF157493) carboxymethylenebutenolidase [Zymomonas mobilis] Length = 310 |
| 250 | 2023250 | Tyr_Phospho_Site(663-671) |
| 251 | 2023251 | Tyr_Phospho_Site(648-655) |
| 252 | 2023252 | 1E-138) >gb AAC62791.1 (AF096371) contains similarity to D-isomer specific 2-hydroxyacid dehydrogenases (Pfam: 2-Hacid_DH.hmm, score: 19.11) [Arabidopsis thaliana] Length = 662 |
| 253 | 2023253 | Tyr_Phospho_Site(984-990) |
| 254 | 2023254 | 1E-130 >sp P42737 CAH2_ARATH CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449 (L18901) carbonic anhydrase [Arabidopsis thaliana] Length = 259 |
| 255 | 2023255 | 1E-135 >emb CAB39787.1 (AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] Length = 280 |
| 256 | 2023256 | Tyr_Phospho_Site(1564-1570) |
| 257 | 2023257 | 1E-140) >gi 3264805 (AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi 4079630 emb CAA10486 (AJ131710) phospho enole |

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| | | pyruvate carboxylase [Arabidopsis thaliana] Length = 968 |
| 258 | 2023258 | 1E-111 >emb CAB10530.1 (Z97343) EREBP-4 like protein [Arabidopsis thaliana] Length = 603 |
| 259 | 2023259 | 1E-127 >sp P48491 TPIS_ARATH TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi 742408 prf 2009415A triose phosphate isomerase [Arabidopsis thaliana] Length = 254 |
| 260 | 2023260 | Tyr_Phospho_Site(963-969) |
| 261 | 2023261 | 1E-152 >emb CAB36755.1 (AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana] Length = 258 |
| 262 | 2023262 | Tyr_Phospho_Site(1080-1087) |
| 263 | 2023263 | 1E-140 >sp Q38997 K110_ARATH SNF1-RELATED PROTEIN KINASE KIN10 (AKIN10) >gi 322596 pir JC1446 serine/threonine protein kinase (EC 2.7.-.-) AK21 - Arabidopsis thaliana >gi 166600 (M93023) SNF1-related protein kinase [Arabidopsis thaliana] >gi 1742969 emb CAA64384 (X94757) ser/thr protein kinase [Arabidopsis thaliana] Length = 512 |
| 264 | 2023264 | 1E-158 >gb AAD28774.1 AF134127_1 (AF134127) Lhcb4.2 protein [Arabidopsis thaliana] Length = 287 |
| 265 | 2023265 | Tyr_Phospho_Site(370-377) |
| 266 | 2023266 | 1E-173 >gb AAD25800.1 AC006550_8 (AC006550) Identical to gb U12536 3-methylcrotonyl-CoA carboxylase precursor protein from Arabidopsis thaliana. ESTs gb H35836, gb AA651295 and gb AA721862 come from this gene. Length = 730 |
| 267 | 2023267 | Tyr_Phospho_Site(861-867) |
| 268 | 2023268 | 1E-131 >gi 3941522 (AF062915) transcription factor [Arabidopsis thaliana] Length = 249 |
| 269 | 2023269 | 1E-147 >gb AAB53256.1 (U66408) GTP-binding protein [Arabidopsis thaliana] >gi 2345150 gb AAB67830 (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana] Length = 399 |
| 270 | 2023270 | Tyr_Phospho_Site(786-793) |
| 271 | 2023271 | 1E-133 >gi 3746809 (AF082882) adenylate kinase [Arabidopsis thaliana] Length = 246 |
| 272 | 2023272 | 3E-91 >emb CAA71277 (Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi 2108254 emb CAA71276 (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi 4538925 emb CAB39661.1 (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana] Length = 1233 |
| 273 | 2023273 | 1E-107 >gi 1353352 (U31975) alanine aminotransferase [Chlamydomonas reinhardtii] Length = 521 |
| 274 | 2023274 | 7E-84 >emb CAA23040.1 (AL035394) receptor kinase [Arabidopsis thaliana] Length = 638 |
| 275 | 2023275 | 1E-129 >gi 1145697 (U39485) delta tonoplast integral protein [Arabidopsis thaliana] Length = 250 |
| 276 | 2023276 | 1E-54 >emb CAA96657.1 (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:... Length = 610 |
| 277 | 2023277 | Pkc_Phospho_Site(73-75) |
| 278 | 2023278 | 1E-154 >gi 3335374 (AC003028) glutaredoxin-like protein [Arabidopsis thaliana] Length = 293 |
| 279 | 2023279 | 1E-128 >gb AAD57005.1 AC009465_19 (AC009465) 40S ribosomal protein S3A (S phase specific) [Arabidopsis thaliana] Length = 262 |
| 280 | 2023280 | 1E-114 >gb AAD28778.1 AF134131_1 (AF134131) PsbS protein [Arabidopsis thaliana] Length = 265 |
| 281 | 2023281 | 7E-62 >gb AAD25756.1 AC007060_14 (AC007060) Contains the PF 00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb T76582, |

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| | | gb N06574 and gb Z25700 come from this gene. [Arabidopsis thaliana] Length = 540 |
| 282 | 2023282 | 0 >sp P25851 F16P_ARATH FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi 99693 pir S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi 11242 emb CAA41154 (X58148) fructose-bisphosphatase [Arabidopsis thaliana] Length = 417 |
| 283 | 2023283 | 1E-162 >gi 4220476 (AC006069) ribophorin I-like protein [Arabidopsis thaliana] Length = 464 |
| 284 | 2023284 | 1E-151 >pir UQPM ubiquitin precursor - garden pea >gi 20589 emb CAA34886 (X17020) polyubiquitin (AA 1-381) [Pisum sativum] >gi 4115339 (L81142) ubiquitin [Pisum sativum] >gi 226707 prf 1603402A polyubiquitin [Pisum sativum] Length = 381 |
| 285 | 2023285 | Rgd(1319-1321) |
| 286 | 2023286 | 1E-143 >gi 3980379 (AC004561) cyclin, PCNA [Arabidopsis thaliana] Length = 264 |
| 287 | 2023287 | 1E-108 >gb AAF00071.1 AF093604_1 (AF093604) apyrase [Arabidopsis thaliana] Length = 471 |
| 288 | 2023288 | 8E-99 >sp P36397 ARF1_ARATH ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi 4630747 gb AAD26597.1 AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana] Length = 181 |
| 289 | 2023289 | Tyr_Phospho_Site(570-577) |
| 290 | 2023290 | Zinc_Finger_C3hc4(177-186) |
| 291 | 2023291 | Pkc_Phospho_Site(23-25) |
| 292 | 2023292 | 1E-146 >emb CAB43632.1 (AL050351) SEC14-like protein [Arabidopsis thaliana] Length = 617 |
| 293 | 2023293 | 1E-109 >sp P46422 GTH4_ARATH GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (GST CLASS PHI) >gi 479736 pir S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi 166723 (L07589) glutathione S-transferase [Arabidopsis thaliana] >gi 347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi 407090 emb CAA53051 (X75303) glutathione S-transferase [Arabidopsis thaliana] >gi 2262152 gb AAC78264.1 AAC78264 (AC002330) Atpm24.1 glutathione S transferase [Arabidopsis thaliana] Length = 212 |
| 294 | 2023294 | 3E-21 >emb CAA22977.1 (AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana] >gi 5732203 emb CAB52678.1 (AJ245908) photosystem I subunit IV precursor [Arabidopsis thaliana] Length = 143 |
| 295 | 2023295 | Tyr_Phospho_Site(441-447) |
| 296 | 2023296 | 1E-159 >gi 166835 (M86720) ribulose biphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi 2642170 (AC003000) Rubisco activase [Arabidopsis thaliana] Length = 446 |
| 297 | 2023297 | Tyr_Phospho_Site(757-764) |
| 298 | 2023298 | 1E-22 >gi 4102690 (AF004806) 24 kDa seed maturation protein [Glycine max] Length = 212 |
| 299 | 2023299 | Tyr_Phospho_Site(366-373) |
| 300 | 2023300 | 1E-142 >gi 4056500 (AC005896) acetyltransferase [Arabidopsis thaliana] Length = 432 |
| 301 | 2023301 | 5E-68 >emb CAA07236 (AJ006771) beta-galactosidase [Cicer arietinum] Length = 707 |
| 302 | 2023302 | 1E-104 >sp P52577 IFRH_ARATH ISOFLAVONE REDUCTASE HOMOLOG P3 >gi 1361992 pir S57613 isoflavonoid reductase homolog - Arabidopsis thaliana |

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| | | >gi 886432 emb CAA89859 (Z49777) isoflavonoid reductase homologue [Arabidopsis thaliana] |
| 303 | 2023303 | 1E-123 >gb AAD20405 (AC007019) ATP synthase [Arabidopsis thaliana] Length = 240 |
| 304 | 2023304 | 1E-131 >dbj BAA32418 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana] Length = 266 |
| 305 | 2023305 | 1E-142 >dbj BAA78560.1 (AB024282) cysteine synthase [Arabidopsis thaliana] >gi 5824334 emb CAB54830.1 (AJ010505) cysteine synthase [Arabidopsis thaliana] Length = 368 |
| 306 | 2023306 | Tyr Phospho Site(92-100) |
| 307 | 2023307 | 2E-79 >emb CAB42925.1 (AL049862) tRNA synthetase [Arabidopsis thaliana] Length = 225 |
| 308 | 2023308 | 3E-25 >gb AAD46141.1 AF081022_1 (AF081022) hypoxia-induced protein L31 [Lycopersicon esculentum] Length = 78 |
| 309 | 2023309 | 1E-110 >emb CAA16677 (AL021684) LRR-like protein [Arabidopsis thaliana] Length = 445 |
| 310 | 2023310 | 8E-38 >dbj BAA22374 (D86122) Mei2-like protein [Arabidopsis thaliana] Length = 884 |
| 311 | 2023311 | 1E-135 >gb AAD32291.1 AC006533_15 (AC006533) acetolactate synthase [Arabidopsis thaliana] Length = 484 |
| 312 | 2023312 | 2E-98 >gb AAB51567.1 (U75189) germin-like protein [Arabidopsis thaliana] >gi 1755158 gb AAB51568.1 (U75190) germin-like protein [Arabidopsis thaliana] >gi 1755170 gb AAB51574.1 (U75196) germin-like protein [Arabidopsis thaliana] >gi 1755172 gb AAB51575.1 (U75197) germin-like protein [Arabidopsis thaliana] >gi 1755180 gb AAB51579.1 (U75201) germin-like protein [Arabidopsis thaliana] >gi 1755190 gb AAB51584.1 (U75206) germin-like protein [Arabidopsis thaliana] >gi 1934728 gb AAB51751.1 (U95035) germin-like protein [Arabidopsis thaliana] >gi 4154285 (AF090733) germin-like protein 1 [Arabidopsis thaliana] >gi 4666248 dbj BAA77207.1 (D89055) germin-like protein precursor [Arabidopsis thaliana] Length = 208 |
| 313 | 2023313 | Pkc Phospho Site(14-16) |
| 314 | 2023314 | Pkc Phospho Site(92-94) |
| 315 | 2023315 | 1E-119 >emb CAA96434 (Z71752) pectin methylesterase [Nicotiana glauca] Length = 315 |
| 316 | 2023316 | 1E-130) >sp O23708 PRC3_ARATH PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3) >gi 2511574 emb CAA73619.1 (Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi 3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana] >gi 4966368 gb AAD34699.1 AC006341_27 (AC006341) Identical to gb Y13176 Arabidopsis thaliana mRNA for proteasome subunit prc3. ESTs gb H36972, gb T22551 and gb T13800 come from this gene. Length = 235 |
| 317 | 2023317 | Pkc Phospho Site(11-13) |
| 318 | 2023318 | Tyr Phospho Site(1345-1353) |
| 319 | 2023319 | Tyr Phospho Site(309-315) |
| 320 | 2023320 | 1E-115 >gi 2829275 (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi 3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1 (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana] Length = 238 |
| 321 | 2023321 | 1E-160 >sp P42498 PHYE_ARATH PHYTOCHROME E >gi 1076376 pir S46313 phytochrome E - Arabidopsis thaliana >gi 452817 emb CAA54075 (X76610) phytochrome E [Arabidopsis thaliana] >gi 5816999 emb CAB53654.1 (AL110123) phytochrome E [Arabidopsis thaliana] Length = 1112 |

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| 322 | 2023322 | 1E-35 >gb AAD28506.1 AF123265_1 (AF123265) remorin 1 [<i>Lycopersicon esculentum</i>] Length = 197 |
| 323 | 2023323 | 1E-171 >gi 4220452 (AC006216) Similar to gi 3413714 T19L18.21 myrosinase-binding protein from <i>Arabidopsis thaliana</i> BAC gb AC004747. ESTs gb T44298, gb T42447, gb R64761 and gb I100206 come from this gene. [<i>Arabidopsis thaliana</i>] Length = 292 |
| 324 | 2023324 | 3E-21 >pir S62011 PHO85 protein - yeast (<i>Saccharomyces cerevisiae</i>) >gi 1163103 (U43503) Lph16p [<i>Saccharomyces cerevisiae</i>] Length = 1223 |
| 325 | 2023325 | 4E-59 >sp P73839 THDF_SYNY3 POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF >gi 1652979 dbj BAA17896 (D90910) thiophen and furan oxidation protein [<i>Synechocystis</i> sp.] Length = 456 |
| 326 | 2023326 | 1E-117 >emb CAA17161 (AL021890) calcium-dependent protein kinase - like protein [<i>Arabidopsis thaliana</i>] >gi 2961339 emb CAA18097.1 (AL022140) calcium-dependent protein kinase-like protein [<i>Arabidopsis thaliana</i>] Length = 554 |
| 327 | 2023327 | 1E-105 >gi 3980412 (AC004561) pumilio-like protein [<i>Arabidopsis thaliana</i>] Length = 968 |
| 328 | 2023328 | 1E-160 >dbj BAA82066.1 (AB022327) nClpP2 [<i>Arabidopsis thaliana</i>] Length = 279 |
| 329 | 2023329 | 1E-129 >emb CAA04172 (AJ000539) phosphatidylinositol synthase [<i>Arabidopsis thaliana</i>] Length = 227 |
| 330 | 2023330 | 8E-65 >gb AAD11598.1 AAD11598 (AF071527) calcium channel [<i>Arabidopsis thaliana</i>] >gi 4263043 gb AAD15312 (AC005142) calcium channel [<i>Arabidopsis thaliana</i>] Length = 724 |
| 331 | 2023331 | Tyr Phospho Site(46-53) |
| 332 | 2023332 | 1E-126 >gi 2981475 (AF053084) cinnamyl alcohol dehydrogenase [<i>Malus domestica</i>] Length = 325 |
| 333 | 2023333 | Tyr Phospho Site(126-132) |
| 334 | 2023334 | 1E-142 >emb CAB39936.1 (AL049500) osmotin precursor [<i>Arabidopsis thaliana</i>] Length = 244 |
| 335 | 2023335 | 1E-138 >gb AAD28767.1 AF134120_1 (AF134120) Lhca2 protein [<i>Arabidopsis thaliana</i>] Length = 257 |
| 336 | 2023336 | Tyr Phospho Site(628-636) |
| 337 | 2023337 | 3E-14 >sp P34092 MYSB_DICDI MYOSIN IB HEAVY CHAIN >gi 102252 pir A33284 myosin heavy chain IB - slime mold (<i>Dictyostelium discoideum</i>) >gi 167839 (M26037) myosin I heavy chain [<i>Dictyostelium discoideum</i>] Length = 1111 |
| 338 | 2023338 | 2E-68 >sp P37707 B2_DAUCA B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot >gi 297889 emb CAA51078 (X72385) B2 protein [<i>Daucus carota</i>] Length = 207 |
| 339 | 2023339 | 1E-146 >gi 3980402 (AC004561) tropinone reductase [<i>Arabidopsis thaliana</i>] Length = 260 |
| 340 | 2023340 | 1E-68 >dbj BAA11226 (D78151) human 26S proteasome subunit p97 [<i>Homo sapiens</i>] Length = 908 |
| 341 | 2023341 | 1E-117 >sp P51430 RS6_ARATH 40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052) ribosomal protein S6 [<i>Arabidopsis thaliana</i>] Length = 249 |
| 342 | 2023342 | 1E-109 >emb CAA17550 (AL021961) receptor protein kinase - like protein [<i>Arabidopsis thaliana</i>] Length = 980 |
| 343 | 2023343 | 1E-106 >sp Q42599 NUIM_ARATH NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi 1076356 pir S52380 NADH dehydrogenase (EC 1.6.99.3) - <i>Arabidopsis thaliana</i> >gi 666977 emb CAA59061 (X84318) NADH dehydrogenase [<i>Arabidopsis thaliana</i>] >gi 3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb X84318 from <i>A.thaliana</i> . ESTs gb Z27005, gb T04711, gb T45078 and gb Z28689 come from this gene. [<i>Arabidopsis thaliana</i>] Length = |

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| | | 222 |
| 344 | 2023344 | 1E-142) >gi 3763918 (AC004450) isopropylmalate dehydratase [Arabidopsis thaliana] Length = 251 |
| 345 | 2023345 | 5E-84 >sp P54641 VATX_DICDI VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum] Length = 356 |
| 346 | 2023346 | 5E-88 >gb AAD15451 (AC006068) receptor protein kinase [Arabidopsis thaliana] Length = 567 |
| 347 | 2023347 | 1E-61 >sp P31166 APT1_ARATH ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi 99657 pir S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi 16164 emb CAA41497 (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi 433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana] Length = 183 |
| 348 | 2023348 | 1E-127 >emb CAA10060.1 (AJ012571) glutathione transferase [Arabidopsis thaliana] Length = 219 |
| 349 | 2023349 | Pkc_Phospho_Site(28-30) |
| 350 | 2023350 | 1E-123 >gi 3201613 (AC004669) glutathione S-transferase [Arabidopsis thaliana] Length = 215 |
| 351 | 2023351 | 1E-109 >sp P51119 GLN2_VITVI GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 2 (GLUTAMATE—AMMONIA LIGASE) >gi 1134898 emb CAA63982 (X94321) glutamine synthetase [Vitis vinifera] Length = 356 |
| 352 | 2023352 | 2E-23 >gi 871782 (L43081) pEARLI 4 gene product [Arabidopsis thaliana] Length = 766 |
| 353 | 2023353 | 1E-150 >emb CAA66963 (X98319) peroxidase [Arabidopsis thaliana] >gi 1429217 emb CAA67311 (X98775) peroxidase ATP12a [Arabidopsis thaliana] Length = 321 |
| 354 | 2023354 | 8E-46 >gi 4206763 (AF104328) cell wall-plasma membrane linker protein homolog [Arabidopsis thaliana] Length = 306 |
| 355 | 2023355 | 1E-140 >gi 1644427 (U74610) glyoxalase II [Arabidopsis thaliana] Length = 256 |
| 356 | 2023356 | 1E-158 >gi 3757514 (AC005167) plasma membrane intrinsic protein [Arabidopsis thaliana] >gi 4581129 gb AAD24619.1 AC005825_26 (AC005825) plasma membrane intrinsic protein [Arabidopsis thaliana] Length = 278 |
| 357 | 2023357 | 1E-139 >gi 2708750 (AC003952) physical impedance protein [Arabidopsis thaliana] Length = 452 |
| 358 | 2023358 | 1E-117 >sp O04157 RAB7_ARATH RAS-RELATED PROTEIN RAB7 >gi 2065015 emb CAA70951 (Y09821) GTP-binding protein Rab7 [Arabidopsis thaliana] >gi 2505866 emb CAA72904 (Y12227) GTP-binding protein Rab7 [Arabidopsis thaliana] >gi 3287684 (AC003979) Strong similarity to gb Y09821 GTP-binding protein Rab7 from A. thaliana. EST gb T76449 comes from this gene. [Arabidopsis thaliana] Length = 203 |
| 359 | 2023359 | 3E-20 >gi 3213227 (AF035209) v-SNARE Vti1a [Mus musculus] >gi 3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus] Length = 217 |
| 360 | 2023360 | 2E-25 >dbj BAA37095.1 (AB022209) ribonucleoprotein F [Rattus norvegicus] Length = 415 |
| 361 | 2023361 | Pkc_Phospho_Site(67-69) |
| 362 | 2023362 | 6E-78 >gb AAD25780.1 AC006577_16 (AC006577) Similar to gb U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF00076 RNA recognition motif domains. ESTs gb T21032 and gb T44127 come from this gene. [Arabidopsis t... Length = 426 |
| 363 | 2023363 | Pkc_Phospho_Site(14-16) |

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| 364 | 2023364 | 3E-11 >emb CAA16558 (AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] Length = 688 |
| 365 | 2023365 | 1E-140 >sp P34791 CYP4_ARATH PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 1076368 pir B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi 405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi 1322278 (U42724) cyclophilin [Arabidopsis thaliana] Length = 260 |
| 366 | 2023366 | 2E-56 >emb CAA89697 (Z49697) cysteine proteinase inhibitor [Ricinus communis] Length = 209 |
| 367 | 2023367 | Tyr Phospho Site(1552-1558) |
| 368 | 2023368 | 1E-137 >gi 2252855 (AF013294) similar to the myc family of helix-loop-helix transcription factors [Arabidopsis thaliana] Length = 423 |
| 369 | 2023369 | 1E-103 >sp P48006 EF1B_ARATH ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi 480620 pir S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi 398608 emb CAA52751 (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana] Length = 231 |
| 370 | 2023370 | 1E-109 >emb CAA74639 (Y14251) glutathione S-transferase [Arabidopsis thaliana] Length = 209 |
| 371 | 2023371 | Rgd(581-583) |
| 372 | 2023372 | 1E-131 >gb AAD51783.1 AF145300_1 (AF145300) 14-3-3 protein GF14 kappa [Arabidopsis thaliana] Length = 248 |
| 373 | 2023373 | 1E-139 >emb CAA51171 (X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana] Length = 251 |
| 374 | 2023374 | Tyr Phospho Site(1037-1044) |
| 375 | 2023375 | 1E-126 >emb CAB10400.1 (Z97340) enoyl-CoA hydratase like protein [Arabidopsis thaliana] Length = 244 |
| 376 | 2023376 | 3E-15 >gb AAD34107.1 AF151870_1 (AF151870) CGI-112 protein [Homo sapiens] Length = 208 |
| 377 | 2023377 | 1E-137 >gb AAD25640.1 AC007170_2 (AC007170) cytoplasmic aconitate hydratase [Arabidopsis thaliana] Length = 898 |
| 378 | 2023378 | Tyr Phospho Site(787-793) |
| 379 | 2023379 | 1E-123 >sp P52032 GSHY_ARATH GLUTATHIONE PEROXIDASE HOMOLOG PRECURSOR >gi 2129599 pir S71250 glutathione peroxidase - Arabidopsis thaliana >gi 1061036 emb CAA61965 (X89866) glutathione peroxidase [Arabidopsis thaliana] Length = 242 |
| 380 | 2023380 | 3E-99 >gb AAD25928.1 AF085279_1 (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana] Length = 570 |
| 381 | 2023381 | 6E-58 >emb CAB43976.1 (AL078579) zinc finger protein [Arabidopsis thaliana] Length = 327 |
| 382 | 2023382 | 1E-132 >gi 3421087 (AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana] >gi 6056394 gb AAF02858.1 AC009324_7 (AC009324) 20S proteasome subunit PAE1 [Arabidopsis thaliana] Length = 237 |
| 383 | 2023383 | 2E-14 >emb CAA92677.1 (Z68315) Similarity to Human MAP kinase phosphatase-1 (SW:PTN7 HUMAN) [Caenorhabditis elegans] Length = 150 |
| 384 | 2023384 | 1E-146 >gb AAD37165.1 AF132742_1 (AF132742) 3-phosphoinositide-dependent protein kinase-1 [Arabidopsis thaliana] Length = 491 |
| 385 | 2023385 | 1E-109 >emb CAA64820 (X95573) salt-tolerance zinc finger protein [Arabidopsis thaliana] Length = 227 |
| 386 | 2023386 | 1E-169 >gi 3834309 (AC005679) Strong similarity to glycoprotein EP1 gb L16983 Daucus carota and a member of S locus glycoprotein family PF 00954. ESTs gb F13813, gb T21052, gb R30218 and gb W43262 come from this gene. |
| 387 | 2023387 | 4E-20 >ref NP_006283.1 PTSG101 tumor susceptibility gene 101 >gi 3184258 (U82130) tumor susceptibility protein [Homo sapiens] Length = 390 |
| 388 | 2023388 | 1E-163 >gi 1046225 (U21952) ethylene response sensor [Arabidopsis |

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| | | thaliana] >gi 2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi 1584365 prf 2122405A ERS gene [Arabidopsis thaliana] Length = 613 |
| 389 | 2023389 | Tyr Phospho Site(86-93) |
| 390 | 2023390 | 1E-138 >sp Q08733 WC1C_ARATH PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi 396218 emb CAA49155 (X69294) transmembrane protein TMP-B [Arabidopsis thaliana] Length = 286 |
| 391 | 2023391 | 7E-28 >dbj BAA32422 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana] Length = 300 |
| 392 | 2023392 | 1E-108 >dbj BAA31509 (AB010877) chloroplast ribosomal protein L3 [Nicotiana tabacum] Length = 259 |
| 393 | 2023393 | Pkc Phospho Site(133-135) |
| 394 | 2023394 | Tyr Phospho Site(1037-1043) |
| 395 | 2023395 | Tyr Phospho Site(603-609) |
| 396 | 2023396 | Tyr Phospho Site(579-586) |
| 397 | 2023397 | 1E-101 >dbj BAA25180 (D88536) delta 9 desaturase [Arabidopsis thaliana] Length = 305 |
| 398 | 2023398 | Tyr Phospho Site(1372-1378) |
| 399 | 2023399 | 1E-105 >emb CAB08077 (Z94058) pectinesterase [Lycopersicon esculentum] Length = 504 |
| 400 | 2023400 | 4E-35 >emb CAA19765 (AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi 3435094 gb AAD12769.1 (AF033586) 9G8-like SR protein [Arabidopsis thaliana] Length = 200 |
| 401 | 2023401 | 1E-125 >gi 2191150 (AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana] Length = 352 |
| 402 | 2023402 | 1E-136 >emb CAA74025.1 (Y13691) multicatalytic endopeptidase complex, proteasome component, alpha subunit [Arabidopsis thaliana] Length = 245 |
| 403 | 2023403 | 1E-156 >sp P25697 KPPR_ARATH PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi 99744 pir S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi 16441 emb CAA41155 (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana] Length = 395 |
| 404 | 2023404 | 1E-90 >dbj BAA77837.1 (AB027458) ACE [Arabidopsis thaliana] >gi 5903086 gb AAD55644.1 AC008017_17 (AC008017) ACE [Arabidopsis thaliana] Length = 594 |
| 405 | 2023405 | 1E-98 >dbj BAA24804 (AB010946) AtRer1B [Arabidopsis thaliana] Length = 195 |
| 406 | 2023406 | Tyr Phospho Site(120-126) |
| 407 | 2023407 | 1E-143 >gb AAD39331.1 AC007258_20 (AC007258) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana] Length = 389 |
| 408 | 2023408 | Tyr Phospho Site(593-601) |
| 409 | 2023409 | 1E-14 >gi 3152583 (AC002986) Contains similarity to inhibitor of apoptosis protein gb U45881 from D. melanogaster. [Arabidopsis thaliana] Length = 347 |
| 410 | 2023410 | Tyr Phospho Site(1596-1603) |
| 411 | 2023411 | Tyr Phospho Site(1068-1075) |
| 412 | 2023412 | 1E-127 >gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] Length = 1203 |
| 413 | 2023413 | 1E-123 >gi 2583123 (AC002387) nucleotide sugar epimerase [Arabidopsis thaliana] Length = 437 |
| 414 | 2023414 | 1E-127 >gb AAD28780.1 AF134133_1 (AF134133) Lil3 protein [Arabidopsis |

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| | | thaliana] Length = 262 |
| 415 | 2023415 | 3E-94 >gi 2511546 (AF022658) c2h2 zinc finger transcription factor [Arabidopsis thaliana] Length = 238 |
| 416 | 2023416 | Tyr_Phospho_Site(724-732) |
| 417 | 2023417 | 1E-123 >gi 2618723 (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi 4389514 gb AAB70451 (AC000104) Identical to Arabidopsis gb AF040632 and gb U49073 IAA17/AXR3 gene. ESTs gb H36782 and gb F14074 come from this gene. [Arabidopsis thaliana] Length = 229 |
| 418 | 2023418 | 1E-157 >gi 4138855 (AF098072) IMMUTANS [Arabidopsis thaliana] Length = 351 |
| 419 | 2023419 | Tyr_Phospho_Site(1298-1305) |
| 420 | 2023420 | 3E-41 >gb AAD45585.1 AF132115_1 (AF132115) cytochrome b-561 [Arabidopsis thaliana] Length = 230 |
| 421 | 2023421 | 1E-127 >pir S25435 chlorophyll a/b-binding protein - Arabidopsis thaliana >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi 166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana] Length = 241 |
| 422 | 2023422 | 1E-148 >sp P21216 IPYR_ARATH SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi 81645 pir S13379 inorganic pyrophosphatase (EC 3.6.1.1) - Arabidopsis thaliana >gi 16348 emb CAA40764 (X57545) inorganic pyrophosphatase [Arabidopsis thaliana] Length = 263 |
| 423 | 2023423 | 8E-69 >gi 3928094 (AC005770) zinc finger protein [Arabidopsis thaliana] Length = 270 |
| 424 | 2023424 | 2E-57 >emb CAA77089 (Y18227) blue copper binding-like protein [Arabidopsis thaliana] Length = 196 |
| 425 | 2023425 | 1E-149 >emb CAA18252.1 (AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana] Length = 992 |
| 426 | 2023426 | Tyr_Phospho_Site(935-942) |
| 427 | 2023427 | 1E-157 >gb AAD18142 (AC006260) plasma membrane intrinsic protein 2B [Arabidopsis thaliana] Length = 285 |
| 428 | 2023428 | Tyr_Phospho_Site(699-707) |
| 429 | 2023429 | 1E-125) >gb AAD24640.1 AC006919_18 (AC006919) pyruvate kinase [Arabidopsis thaliana] Length = 464 |
| 430 | 2023430 | Rgd(1781-1783) |
| 431 | 2023431 | 1E-134 >gb AAD24630.1 AC006919_8 (AC006919) fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana] Length = 358 |
| 432 | 2023432 | Pkc_Phospho_Site(101-103) |
| 433 | 2023433 | 1E-136 >gi 3004557 (AC003673) plasma membrane proton pump H ⁺ ATPase, PMA1 [Arabidopsis thaliana] Length = 949 |
| 434 | 2023434 | 1E-138) >gi 2191128 (AF007269) belongs to the L5P family of ribosomal proteins [Arabidopsis thaliana] Length = 262 |
| 435 | 2023435 | 3E-98 >gi 1946371 (U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana] Length = 780 |
| 436 | 2023436 | 1E-156 >gb AAD28773.1 AF134126_1 (AF134126) Lhcb3 protein [Arabidopsis thaliana] >gi 5002210 gb AAD37362.1 AF143691_1 (AF143691) type III chlorophyll a/b binding protein [Arabidopsis thaliana] Length = 265 |
| 437 | 2023437 | 7E-67 >gi 2459430 (AC002332) CUC2 protein [Arabidopsis thaliana] Length = 268 |
| 438 | 2023438 | 1E-155 >sp P04777 CB21_ARATH CHLOROPHYLL A-B BINDING PROTEIN 165/180 PRECURSOR (LHCII TYPE I CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding protein (LHCP AB 65) |

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| | | [Arabidopsis thaliana] >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] Length = 267 |
| 439 | 2023439 | 2E-58 >emb CAA63223 (X92491) TOM20 [Solanum tuberosum] Length = 204 |
| 440 | 2023440 | 1E-89 >emb CAB40742.1 (AJ237751) aquaglyceroporin [Nicotiana tabacum] Length = 247 |
| 441 | 2023441 | 1E-29 >gb AAD15610 (AC006232) selenium-binding protein [Arabidopsis thaliana] Length = 472 |
| 442 | 2023442 | 1E-146) >gb AAD20124 (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana] Length = 258 |
| 443 | 2023443 | 1E-125 >emb CAB45800.1 (AL080252) nodulin-like protein [Arabidopsis thaliana] Length = 368 |
| 444 | 2023444 | Tyr_Phospho_Site(880-887) |
| 445 | 2023445 | Tyr_Phospho_Site(747-754) |
| 446 | 2023446 | Tyr_Phospho_Site(353-361) |
| 447 | 2023447 | 4E-34 >gi 3421373 (AF079901) 28 kDa cis-Golgi SNARE [Mus musculus] Length = 250 |
| 448 | 2023448 | 1E-64 >sp Q43794 SYE_TOBAC GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE—TRNA LIGASE) (GLURS) >gi 1084418 pir S51685 glutamate—tRNA ligase (EC 6.1.1.17) - common tobacco >gi 603867 emb CAA58506 (X83524) glutamate—tRNA ligase [Nicotiana tabacum] Length = 569 |
| 449 | 2023449 | 1E-110 >emb CAB16805.1 (Z99708) minor allergen [Arabidopsis thaliana] Length = 273 |
| 450 | 2023450 | 6E-17 >gb AAD25848.1 AC007197_1 (AC007197) disease resistance gene, 5' partial [Arabidopsis thaliana] Length = 554 |
| 451 | 2023451 | 1E-65 >emb CAA74639 (Y14251) glutathione S-transferase [Arabidopsis thaliana] Length = 209 |
| 452 | 2023452 | 2E-83 >gi 2598932 (AF027157) auxin-responsive protein IAA2 [Arabidopsis thaliana] Length = 174 |
| 453 | 2023453 | 8E-56 >gi 3287683 (AC003979) Similar to apoptosis protein MA-3 gb D50465 from Mus musculus. [Arabidopsis thaliana] Length = 693 |
| 454 | 2023454 | 1E-125) >gi 1764100 (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis thaliana] Length = 373 |
| 455 | 2023455 | 1E-109 >gi 3510259 (AC005310) inorganic pyrophosphatase [Arabidopsis thaliana] >gi 3522960 gb AAC34242.1 (AC004411) inorganic pyrophosphatase [Arabidopsis thaliana] Length = 216 |
| 456 | 2023456 | 2E-20 >emb CAA07361.1 (AJ006972) TOM1 [Mus musculus] Length = 492 |
| 457 | 2023457 | 1E-143 >gb AAD25595.1 AC007211_17 (AC007211) chlorophyll A/B binding protein [Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana] Length = 265 |
| 458 | 2023458 | 1E-79) >gb AAD31350.1 AC007212_6 (AC007212) bZIP transcription factor [Arabidopsis thaliana] Length = 171 |
| 459 | 2023459 | Pkc_Phospho_Site(2-4) |
| 460 | 2023460 | Pkc_Phospho_Site(9-11) |
| 461 | 2023461 | 1E-146 >gi 3980396 (AC004561) C-4 sterol methyl oxidase [Arabidopsis thaliana] Length = 253 |
| 462 | 2023462 | Tyr_Phospho_Site(620-626) |
| 463 | 2023463 | 6E-81) >gi 3831468 (AC005700) phosphocholine cytidyltransferase [Arabidopsis thaliana] >gi 5640001 gb AAD45922.1 AF165912_1 (AF165912) CTP:phosphocholine cytidyltransferase [Arabidopsis thaliana] Length = 332 |
| 464 | 2023464 | 1E-153 >gi 3850579 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 an... Length = 433 |

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| 465 | 2023465 | 1E-40 >sp P48724 IF5_PHAVU EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi 1008881 (L47221) eukaryotic initiation factor 5 [Phaseolus vulgaris] Length = 443 |
| 466 | 2023466 | 2E-96 >sp P42043 HMZ1_ARATH FERROCHELATASE I, CHLOROPLAST/MITOCHONDRIAL PRECURSOR (PROTOHEME FERROLYASE) (HEME SYNTHETASE) >gi 1076325 pir A54125 ferrochelatase (EC 4.99.1.1) precursor, chloroplast - Arabidopsis thaliana >gi 511081 emb CAA51819 (X73417) ferrochelatase [Arabid |
| 467 | 2023467 | Pkc Phospho_Site(8-10) |
| 468 | 2023468 | 1E-132 >dbj BAA31525 (AB013301) ethylene responsive element binding factor [Arabidopsis thaliana] Length = 281 |
| 469 | 2023469 | 1E-112) >sp P28187 ARA4_ARATH RAS-RELATED PROTEIN ARA-4 >gi 81633 pir JS0641 GTP-binding protein ara-4 - Arabidopsis thaliana >gi 217839 dbj BAA00831 (D01026) small GTP-binding protein [Arabidopsis thaliana] >gi 3763922 (AC004450) GTP-binding protein [Arabidopsis thaliana] Length = 214 |
| 470 | 2023470 | Rgd(476-478) |
| 471 | 2023471 | Zinc_Finger_C2h2(514-536) |
| 472 | 2023472 | 2E-92 >gi 1872521 (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi 5262161 emb CAB45804.1 (AL080253) zinc-finger protein Lsd1 [Arabidopsis thaliana] Length = 189 |
| 473 | 2023473 | 1E-133 >emb CAB42872.1 (AJ012423) wall-associated kinase 2 [Arabidopsis thaliana] Length = 732 |
| 474 | 2023474 | 2E-30 >gi 2224911 (U93048) somatic embryogenesis receptor-like kinase [Daucus carota] Length = 553 |
| 475 | 2023475 | Tyr_Phospho_Site(869-875) |
| 476 | 2023476 | 3E-46 >dbj BAA25999 (AB013447) aluminum-induced [Brassica napus] Length = 244 |
| 477 | 2023477 | Rgd(263-265) |
| 478 | 2023478 | 1E-104) >emb CAA70498 (Y09314) Rab2-like protein [Arabidopsis thaliana] >gi 5281023 emb CAB45962.1 (Z97343) GTP-binding RAB2A like protein [Arabidopsis thaliana] Length = 211 |
| 479 | 2023479 | Tyr_Phospho_Site(465-473) |
| 480 | 2023480 | Tyr_Phospho_Site(143-151) |
| 481 | 2023481 | 2E-36 >emb CAB39631.1 (AL049481) DNA-directed RNA polymerase [Arabidopsis thaliana] Length = 748 |
| 482 | 2023482 | 8E-28 >dbj BAA76626.1 (AB019392) muscle specific gene M9 [Homo sapiens] >gi 4689150 gb AAD27784.1 AF077051_1 (AF077051) PTD001 [Homo sapiens] Length = 218 |
| 483 | 2023483 | 1E-148 >gi 3249095 (AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb L13703 from Schizosaccharomyces pombe. ESTs gb N37567 and gb T43002 come from this gene. [Arabidopsis thaliana] Length = 550 |
| 484 | 2023484 | 1E-111 >gi 3746809 (AF082882) adenylate kinase [Arabidopsis thaliana] Length = 246 |
| 485 | 2023485 | Tyr_Phospho_Site(370-378) |
| 486 | 2023486 | 7E-61 >gi 549975 (U12858) nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707 [Arabidopsis thaliana] Length = 382 |
| 487 | 2023487 | 1E-105 >sp Q96283 RB1A_ARATH RAS-RELATED PROTEIN RAB11A >gi 2598229 emb CAA70112 (Y08904) Rab11 protein [Arabidopsis thaliana] >gi 5541676 emb CAB51182.1 (AL096859) Rab11 protein [Arabidopsis thaliana] Length = 217 |
| 488 | 2023488 | 4E-89 >gb AAD25137.1 AC007127_3 (AC007127) ubiquitin protein [Arabidopsis thaliana] Length = 536 |

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| 489 | 2023489 | Zinc Finger C2h2(1776-1798) |
| 490 | 2023490 | 1E-112 >gi 2191174 (AF007270) similar to the peptidase family S16 [Arabidopsis thaliana] Length = 1096 |
| 491 | 2023491 | 1E-147 >gi 3461837 (AC005315) expansin [Arabidopsis thaliana] >gi 3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana] Length = 257 |
| 492 | 2023492 | 1E-173 >gi 3157937 (AC002131) Identical to aspartic proteinase cDNA gb U51036 from A. thaliana. ESTs gb N96313, gb T21893, gb R30158, gb T21482, gb T43650, gb R64749, gb R65157, gb T88269, gb T44552, gb T22542, gb T76533, gb T44350, gb Z34591, gb AA728734, gb... Length = 506 |
| 493 | 2023493 | 4E-43 >dbj BAA25989 (D89051) ERD6 protein [Arabidopsis thaliana] Length = 496 |
| 494 | 2023494 | Tyr Phospho Site(419-426) |
| 495 | 2023495 | Tyr Phospho Site(1183-1190) |
| 496 | 2023496 | 1E-162 >emb CAA71627 (Y10617) 12-oxophytodienoate reductase [Arabidopsis thaliana] Length = 370 |
| 497 | 2023497 | Tyr Phospho Site(1175-1181) |
| 498 | 2023498 | Pkc Phospho Site(18-20) |
| 499 | 2023499 | 1E-12 >gi 3834382 (AF033109) syntaxin 8 [Rattus norvegicus] Length = 236 |
| 500 | 2023500 | 1E-132 >gi 2317729 (AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana] Length = 357 |
| 501 | 2023501 | 9E-93 >sp P34091 RL6_MESCR 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586 ribosomal protein ML16 - common ice plant >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum] Length = |
| 502 | 2023502 | Pkc Phospho Site(26-28) |
| 503 | 2023503 | 3E-11 >gi 4100433 (AF000378) beta-glucosidase [Glycine max] Length = 206 |
| 504 | 2023504 | Tyr Phospho Site(1044-1050) |
| 505 | 2023505 | Tyr Phospho Site(659-666) |
| 506 | 2023506 | 4E-66 >gi 2443890 (AC002294) similar to NAM (gp X92205 1321924) and CUC2 (gp AB002560 1944132) proteins [Arabidopsis thaliana] Length = 300 |
| 507 | 2023507 | 8E-24 >gi 3608412 (AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum] Length = 309 |
| 508 | 2023508 | Tyr Phospho Site(392-398) |
| 509 | 2023509 | Tyr Phospho Site(184-191) |
| 510 | 2023510 | Tyr Phospho Site(877-883) |
| 511 | 2023511 | 8E-22 >gi 2622711 (AE000918) ferripyochelin binding protein [Methanobacterium thermoautotrophicum] Length = 151 |
| 512 | 2023512 | Pkc Phospho Site(11-13) |
| 513 | 2023513 | 2E-20 >ref NP_005998.1 PZNF216 zinc finger protein 216 >gi 3643809 (AF062346) zinc finger protein 216 splice variant 1 [Homo sapiens] >gi 3643811 (AF062347) zinc finger protein 216 splice variant 2 [Homo sapiens] >gi 3668066 gb AAC61801.1 (AF062072) zinc finger protein 216 [Homo sapiens] Length = 213 |
| 514 | 2023514 | Pkc Phospho Site(29-31) |
| 515 | 2023515 | 1E-103 >sp Q38912 RAC3_ARATH RAC-LIKE GTP BINDING PROTEIN ARAC3 >gi 1304413 (U43501) Rac-like protein [Arabidopsis thaliana] >gi 2645643 (AF031427) Rho-like GTP binding protein [Arabidopsis thaliana] >gi 2924513 emb CAA17767.1 (AL022023) Rho1Ps homolog/ Rac-like protein [Arabido |
| 516 | 2023516 | 4E-46 >emb CAA72716 (Y11987) FPF1 protein [Sinapis alba] Length = 110 |
| 517 | 2023517 | 1E-119 >emb CAB45987.1 (AL080318) stress-induced protein sti1-like protein [Arabidopsis thaliana] Length = 558 |

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| 518 | 2023518 | 1E-145 >gi 3980379 (AC004561) cyclin, PCNA [Arabidopsis thaliana] Length = 264 |
| 519 | 2023519 | 1E-66 >emb CAB16514.1 (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes |
| 520 | 2023520 | Pkc_Phospho_Site(26-28) |
| 521 | 2023521 | 2E-45 >emb CAA74401.1 (Y14072) HMG protein [Arabidopsis thaliana] Length = 144 |
| 522 | 2023522 | 4E-40 >pir S62699 photoassimilate-responsive protein PAR-1b precursor - common tobacco >gi 871487 emb CAA58731 (X83851) mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Ni |
| 523 | 2023523 | Pkc_Phospho_Site(165-167) |
| 524 | 2023524 | 2E-60 >gi 3600061 (AF080120) contains similarity to DNA binding proteins [Arabidopsis thaliana] >gi 4850286 emb CAB43042.1 (AL049876) protein [Arabidopsis thaliana] Length = 313 |
| 525 | 2023525 | 7E-42 >gi 3789911 (AF081802) developmental protein DG1118 [Dictyostelium discoideum] Length = 192 |
| 526 | 2023526 | Tyr_Phospho_Site(2-8) |
| 527 | 2023527 | Tyr_Phospho_Site(248-254) |
| 528 | 2023528 | Pkc_Phospho_Site(85-87) |
| 529 | 2023529 | 1E-125 >sp P28188 ARA5_ARATH RAS-RELATED PROTEIN ARA-5 >gi 2317906 (U89959) ARA-5 [Arabidopsis thaliana] Length = 258 |
| 530 | 2023530 | Zinc_Protease(1367-1376) |
| 531 | 2023531 | 1E-127 >gb AAD30573.1 AC007260_4 (AC007260) 50S Ribosomal protein L13 [Arabidopsis thaliana] Length = 241 |
| 532 | 2023532 | Pkc_Phospho_Site(53-55) |
| 533 | 2023533 | 4E-57 >sp O23760 COMT_CLABR CAFFEIC ACID 3-O- METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O- METHYLTRANSFERASE) (COMT) >gi 2240207 (AF006009) caffeic acid O- methyltransferase [Clarkia breweri] Length = 370 |
| 534 | 2023534 | Tyr_Phospho_Site(884-892) |
| 535 | 2023535 | Pkc_Phospho_Site(55-57) |
| 536 | 2023536 | 6E-16 >gi 2281649 (AF003105) AP2 domain containing protein RAP2.12 [Arabidopsis thaliana] Length = 317 |
| 537 | 2023537 | 6E-34 >emb CAB39533.1 (AJ223758) 54 kDa vacuolar H(+)-ATPase subunit [Sus scrofa] Length = 483 |
| 538 | 2023538 | 3E-19 >ref NP_005998.1 PZNF216 zinc finger protein 216 >gi 3643809 (AF062346) zinc finger protein 216 splice variant 1 [Homo sapiens] >gi 3643811 (AF062347) zinc finger protein 216 splice variant 2 [Homo sapiens] >gi 3668066 gb AAC61801.1 (AF062072) zinc finger protein 216 [Homo sapiens] Length = 213 |
| 539 | 2023539 | Zinc_Finger_C3hc4(1254-1263) |
| 540 | 2023540 | 8E-43 >emb CAB40041.1 (AL049524) alpha NAC [Arabidopsis thaliana] Length = 212 |
| 541 | 2023541 | 3E-64 >emb CAB53477.1 (AJ245900) CAA30374.1 protein [Oryza sativa] Length = 603 |
| 542 | 2023542 | 1E-93 >pir S42651 hypothetical protein - rape >gi 6065752 emb CAB58175.1 (X74225) pod-specific dehydrogenase SAC25 [Brassica napus] Length = 320 |
| 543 | 2023543 | 1E-139 >gb AAD25850.1 AC007197_3 (AC007197) cytochrome p450 [Arabidopsis thaliana] Length = 518 |
| 544 | 2023544 | 1E-124 >emb CAA65988 (X97323) outward rectifying potassium channel KCO1 [Arabidopsis thaliana] >gi 2230761 emb CAA69158 (Y07825) kco1 [Arabidopsis thaliana] Length = 363 |

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| 545 | 2023545 | Tyr_Phospho_Site(258-265) |
| 546 | 2023546 | 9E-38 >emb CAA74000 (Y13649) homologous to GATA-binding transcription factors [Arabidopsis thaliana] >gi 4895246 gb AAD32831.1 AC007659_13 (AC007659) GATA-binding transcription factor [Arabidopsis thaliana] Le |
| 547 | 2023547 | 1E-124 >gb AAD02810 (AF062396) protein phosphatase 2A regulatory subunit isoform B' delta [Arabidopsis thaliana] Length = 477 |
| 548 | 2023548 | Tyr_Phospho_Site(4-11) |
| 549 | 2023549 | 1E-32 >dbj BAA22813 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] Length = 502 |
| 550 | 2023550 | 1E-105 >gi 3860277 (AC005824) ribosomal protein L10 [Arabidopsis thaliana] >gi 4314394 gb AAD15604 (AC006232) ribosomal protein L10A [Arabidopsis thaliana] Length = 222 |
| 551 | 2023551 | 5E-42 >gb AAD43442.1 AF107837_1 (AF107837) 26S proteasome subunit p40.5 [Homo sapiens] Length = 376 |
| 552 | 2023552 | 1E-68 >emb CAB36757.1 (AL035523) acid phosphatase-like protein [Arabidopsis thaliana] Length = 260 |
| 553 | 2023553 | Pkc_Phospho_Site(21-23) |
| 554 | 2023554 | 0) >gi 3482924 (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana] Length = 322 |
| 555 | 2023555 | 4E-94 >gb AAD50055.1 AC007980_20 (AC007980) ATP-dependent metalloprotease [Arabidopsis thaliana] Length = 716 |
| 556 | 2023556 | Tyr_Phospho_Site(1518-1526) |
| 557 | 2023557 | Tyr_Phospho_Site(254-262) |
| 558 | 2023558 | 2E-25 >sp P35559 IDE_RAT INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE) >gi 347022 pir S29509 insulinase (EC 3.4.99.45) - rat >gi 56492 emb CAA47689 (X67269) insulin-degrading enzyme [Rattus norvegicus] |
| 559 | 2023559 | 1E-44 >emb CAA74400.1 (Y14071) HMG protein [Arabidopsis thaliana] >gi 3068715 (AF049236) unknown [Arabidopsis thaliana] Length = 178 |
| 560 | 2023560 | 1E-109 >gi 2281647 (AF003104) AP2 domain containing protein RAP2.11 [Arabidopsis thaliana] Length = 255 |
| 561 | 2023561 | Tyr_Phospho_Site(300-308) |
| 562 | 2023562 | Pkc_Phospho_Site(62-64) |
| 563 | 2023563 | 9E-61 >emb CAA71502 (Y10477) chloroplast thylakoidal processing peptidase [Arabidopsis thaliana] Length = 340 |
| 564 | 2023564 | Tyr_Phospho_Site(685-692) |
| 565 | 2023565 | 1E-12 >gi 3287691 (AC003979) Contains similarity to RING zinc finger protein gb X95455 from Gallus gallus. [Arabidopsis thaliana] Length = 398 |
| 566 | 2023566 | Rgd(902-904) |
| 567 | 2023567 | Rgd(1696-1698) |
| 568 | 2023568 | 4E-41 >gi 2462833 (AF000657) highly similar to froha and frohb, potential frohc, tumor related protein [Arabidopsis thaliana] Length = 693 |
| 569 | 2023569 | Pkc_Phospho_Site(8-10) |
| 570 | 2023570 | Tyr_Phospho_Site(1252-1259) |
| 571 | 2023571 | 3E-22 >gi 4091808 (AF053307) deacetyl/vindoline 4-O-acetyltransferase [Catharanthus roseus] Length = 439 |
| 572 | 2023572 | 1E-142 >sp P48422 C861_ARATH CYTOCHROME P450 86A1 (CYPLXXXVI) >gi 940446 emb CAA62082 (X90458) cytochrome p450 [Arabidopsis thaliana] Length = 513 |
| 573 | 2023573 | 1E-130) >gb AAD50014.1 AC007651_9 (AC007651) glutathione transferase [Arabidopsis thaliana] Length = 220 |
| 574 | 2023574 | 4E-24 >gb AAD33602.1 AF133302_1 (AF133302) type 2 peroxiredoxin [Brassica rapa subsp. pekinensis] Length = 162 |
| 575 | 2023575 | 1E-108 >gi 3860277 (AC005824) ribosomal protein L10 [Arabidopsis |

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| | | thaliana] >gi 4314394 gb AAD15604 (AC006232) ribosomal protein L10A [Arabidopsis thaliana] Length = 222 |
| 576 | 2023576 | Tyr_Phospho_Site(301-308) |
| 577 | 2023577 | 8E-75 >emb CAA17547.1 (AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi 3402748 emb CAA20194.1 (AL031187) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] Length = 223 |
| 578 | 2023578 | Tyr_Phospho_Site(49-56) |
| 579 | 2023579 | 1E-83 >emb CAA18743.1 (AL022604) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana] Length = 367 |
| 580 | 2023580 | Pkc_Phospho_Site(2-4) |
| 581 | 2023581 | 5E-40 >pir S52995 arabinogalactan-like protein - loblolly pine >gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda] Length = 264 |
| 582 | 2023582 | 4E-23 >emb CAA10616 (AJ132240) eukaryotic translation initiation factor 5 [Zea mays] Length = 451 |
| 583 | 2023583 | 2E-65 >sp P29545 EF1D_ORYSA ELONGATION FACTOR 1-BETA' (EF-1-BETA') >gi 322851 pir S29224 translation elongation factor eEF-1 beta' chain - rice >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta' [Oryza sativa] Length = 223 |
| 584 | 2023584 | 1E-36 >gb AAF00645.1 AC009540_22 (AC009540) cationic amino acid transporter [Arabidopsis thaliana] Length = 614 |
| 585 | 2023585 | 1E-123 >gi 3152563 (AC002986) Similar to myb-related transcription factors e.g., gb X98308. EST gb T22093 and gb T22697 come from this gene. [Arabidopsis thaliana] Length = 327 |
| 586 | 2023586 | 9E-13 >emb CAB10221.1 (Z97336) elicitor like protein [Arabidopsis thaliana] Length = 158 |
| 587 | 2023587 | 1E-100 >gb AAD35009.1 AF144391_1 (AF144391) thioredoxin-like 5 [Arabidopsis thaliana] Length = 185 |
| 588 | 2023588 | Rgd(1535-1537) |
| 589 | 2023589 | 1E-105 >gi 2262173 (AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana] Length = 383 |
| 590 | 2023590 | Tyr_Phospho_Site(1491-1497) |
| 591 | 2023591 | Tyr_Phospho_Site(966-972) |
| 592 | 2023592 | 2E-56 >sp Q06138 MO25_MOUSE MO25 PROTEIN >gi 2143483 pir I57997 hypothetical calcium-binding protein - mouse >gi 262934 bbs 121784 (S51858) Ca2+ binding protein [mice, embryos, Peptide, 341 aa] [Mus sp.] Length = 341 |
| 593 | 2023593 | 4E-99 >gi 3822225 (AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana] Length = 190 |
| 594 | 2023594 | 5E-98 >dbj BAA31144 (AB010916) response reactor2 [Arabidopsis thaliana] >gi 4678318 emb CAB41129.1 (AL049658) response reactor2 [Arabidopsis thaliana] Length = 184 |
| 595 | 2023595 | 1E-122 >gi 1046225 (U21952) ethylene response sensor [Arabidopsis thaliana] >gi 2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi 1584365 prf 2122405A ERS gene [Arabidopsis thaliana] Length = 613 |
| 596 | 2023596 | 3E-28 >gi 2494114 (AC002376) Contains similarity to Daucus glycine-rich cell wall protein (gb D29974). EST gb R29840 comes from this gene. [Arabidopsis thaliana] Length = 212 |
| 597 | 2023597 | Tyr_Phospho_Site(780-786) |
| 598 | 2023598 | 2E-80 >emb CAA09198 (AJ010459) RNA helicase [Arabidopsis thaliana] Length = 145 |
| 599 | 2023599 | 7E-27 >gb AAD46402.1 AF096246_1 (AF096246) ethylene-responsive transcriptional coactivator [Lycopersicon esculentum] Length = 146 |
| 600 | 2023600 | Pkc_Phospho_Site(151-153) |
| 601 | 2023601 | 2E-82 >gb AAD27618.1 AF124376_1 (AF124376) 30S ribosomal protein S7 |

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| | | [Brassica napus] >gi 5881740 dbj BAA84431.1 (AP000423) ribosomal protein S7 [Arabidopsis thaliana] >gi 5881755 dbj BAA84446.1 (AP000423) ribosomal protein S7 [Arabidopsis thaliana] Length = 155 |
| 602 | 2023602 | 2E-79 >gb AAD14462 (AC005275) glycosylation enzyme [Arabidopsis thaliana] Length = 448 |
| 603 | 2023603 | 4E-98 >dbj BAA74528 (AB016471) ARR1 protein [Arabidopsis thaliana] Length = 669 |
| 604 | 2023604 | 5E-74 >gi 3169883 (AF033194) dehydroquinase dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi 3169888 (AF034411) dehydroquinase dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] Length = 545 |
| 605 | 2023605 | Tyr Phospho Site(382-390) |
| 606 | 2023606 | Tyr Phospho Site(1085-1092) |
| 607 | 2023607 | Tyr Phospho Site(538-545) |
| 608 | 2023608 | 2E-69 >gb AAD21706.1 (AC007048) tyrosine transaminase [Arabidopsis thaliana] Length = 462 |
| 609 | 2023609 | Tyr Phospho Site(216-223) |
| 610 | 2023610 | Pkc Phospho Site(10-12) |
| 611 | 2023611 | 1E-35 >gb AAD45979.1 (AF115334) MenG [Pseudomonas fluorescens] Length = 163 |
| 612 | 2023612 | 9E-23 >dbj BAA32422 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana] Length = 300 |
| 613 | 2023613 | 2E-90 >pir S71219 cytosolic cyclophilin ROC3 - Arabidopsis thaliana >gi 1305455 (U40399) cytosolic cyclophilin [Arabidopsis thaliana] >gi 4581104 gb AAD24594.1 AC005825_1 (AC005825) cytosolic cyclophilin (ROC3) [Arabidopsis thaliana] Length = 173 |
| 614 | 2023614 | Tyr Phospho Site(78-86) |
| 615 | 2023615 | Pkc Phospho Site(12-14) |
| 616 | 2023616 | Tyr Phospho Site(772-780) |
| 617 | 2023617 | 1E-106 >emb CAB45054.1 (AL078637) HSP90-like protein [Arabidopsis thaliana] Length = 823 |
| 618 | 2023618 | 1E-101 >gi 4056469 (AC005990) Strong similarity to gb M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb Z25826, gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967, gb AA712956, gb T46403, gb T46050, gb AI100391 and gb Z25043 come from t... Length = 188 |
| 619 | 2023619 | Tyr Phospho Site(9-16) |
| 620 | 2023620 | 3E-44 >gi 3201632 (AC004669) 2A6 protein [Arabidopsis thaliana] Length = 358 |
| 621 | 2023621 | 1E-113 >emb CAB10222.1 (Z97336) carnitine racemase like protein [Arabidopsis thaliana] Length = 240 |
| 622 | 2023622 | 1E-63 >gi 3341698 (AC003672) blue copper-binding protein II [Arabidopsis thaliana] Length = 202 |
| 623 | 2023623 | 1E-108 >sp Q96558 UGDH SOYBN UDP-GLUCOSE 6-DEHYDROGENASE (UDP-GLC DEHYDROGENASE) (UDP-GLCDH) (UDPGDH) >gi 1518540 (U53418) UDP-glucose dehydrogenase [Glycine max] Length = 480 |
| 624 | 2023624 | Tyr Phospho Site(515-522) |
| 625 | 2023625 | Tyr Phospho Site(1716-1723) |
| 626 | 2023626 | 2E-16 >emb CAA84724.1 (Z35663) similar to ribonucleoprotein; cDNA EST yk222a11.3 comes from this gene; cDNA EST yk222a11.5 comes from this gene; cDNA EST yk432f10.3 comes from this gene; cDNA EST yk432f10.5 comes from this gene; cDNA EST yk497a8.3 ... Length = 307 |
| 627 | 2023627 | 2E-57 >gi 3482933 (AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana] Length = 967 |
| 628 | 2023628 | Tyr Phospho Site(4-12) |
| 629 | 2023629 | 4E-92 >gi 3201969 (AF068332) submergence induced protein 2A [Oryza |

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| | | sativa] Length = 198 |
| 630 | 2023630 | 1E-110 >gb AAD41977.1 AC006438_9 (AC006438) unknown protein [Arabidopsis thaliana] Length = 203 |
| 631 | 2023631 | Tyr Phospho Site(983-990) |
| 632 | 2023632 | 1E-106 >gi 3482931 (AC003970) germin-like protein [Arabidopsis thaliana] Length = 219 |
| 633 | 2023633 | 4E-68 >gi 4193388 (AF091455) translationally controlled tumor protein [Hevea brasiliensis] Length = 168 |
| 634 | 2023634 | 5E-23 >gi 3193325 (AF069299) contains similarity to pectinesterases [Arabidopsis thaliana] Length = 209 |
| 635 | 2023635 | 2E-45 >emb CAB52425.1 (AL109770) similar to yeast vacuolar sorting protein VPS29/PEP11 [Schizosaccharomyces pombe] Length = 187 |
| 636 | 2023636 | 9E-16 >sp P53173 ERV4_YEAST ER-DERIVED VESICLES PROTEIN ERV14 >gi 2132531 pir S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae) >gi 1322550 emb CAA96756 (Z72576) ORF YGL054c [Saccharomyces cerevisiae] Length = 138 |
| 637 | 2023637 | 1E-126 >gi 3415113 (AF081201) villin 1 [Arabidopsis thaliana] Length = 910 |
| 638 | 2023638 | 1E-125 >pir S58282 dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi 928932 emb CAA89205 (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene [Arabidopsis thaliana] Length = 445 |
| 639 | 2023639 | Tyr Phospho Site(1102-1110) |
| 640 | 2023640 | 2E-30 >sp Q01264 HYUC_PSESN HYDANTOIN UTILIZATION PROTEIN C (ORF4) >gi 151284 (M72717) DL-hydantoinase [Pseudomonas sp.] >gi 216833 dbj BAA01379 (D10494) N-carbamyl-L-amino acid amidohydrolase [Pseudomonas sp.] Length = 414 |
| 641 | 2023641 | Tyr Phospho Site(127-134) |
| 642 | 2023642 | Tyr Phospho Site(407-413) |
| 643 | 2023643 | 1E-155 >gb AAD21710.1 (AC007048) protein phosphatase 2C [Arabidopsis thaliana] Length = 290 |
| 644 | 2023644 | 4E-97 >gi 862640 (U20182) MADS-box protein AGL11 [Arabidopsis thaliana] >gi 4538999 emb CAB39620.1 (AL049481) MADS-box protein AGL11 [Arabidopsis thaliana] Length = 230 |
| 645 | 2023645 | 1E-127 >gi 3894171 (AC005312) glutathione s-transferase [Arabidopsis thaliana] Length = 221 |
| 646 | 2023646 | 1E-120 >sp Q39222 RB1B_ARATH RAS-RELATED PROTEIN RAB11 >gi 2118459 pir S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi 451860 (L18883) small GTP-binding protein [Arabidopsis thaliana] Length = 216 |
| 647 | 2023647 | Tyr Phospho Site(162-168) |
| 648 | 2023648 | 7E-29 >dbj BAA22813 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] Length = 502 |
| 649 | 2023649 | 1E-34 >dbj BAA12797 (D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa] Length = 169 |
| 650 | 2023650 | Pkc Phospho Site(60-62) |
| 651 | 2023651 | Tyr Phospho Site(927-934) |
| 652 | 2023652 | 1E-128 >gb AAD20681 (AC006283) similar to protein Htf9C [Arabidopsis thaliana] Length = 850 |
| 653 | 2023653 | 1E-117 >gb AAD22643.1 AC007138_7 (AC007138) protein transport factor [Arabidopsis thaliana] Length = 856 |
| 654 | 2023654 | Tyr Phospho Site(951-957) |
| 655 | 2023655 | Pkc Phospho Site(31-33) |
| 656 | 2023656 | 8E-23 >emb CAB50433.1 (AJ248287) hypothetical DEHYDROGENASE [Pyrococcus abyssi] Length = 333 |

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| 657 | 2023657 | 1E-129 >sp Q08770 RL10_ARATH 60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi 478401 pir JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi 17682 emb CAA78856 (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana] Length = 220 |
| 658 | 2023658 | 6E-22 >gb AAD32844.1 AC007658_3 (AC007658) thioredoxin-like protein [Arabidopsis thaliana] Length = 130 |
| 659 | 2023659 | 1E-141 >emb CAB41166.1 (AL049659) cytochrome P450-like protein [Arabidopsis thaliana] Length = 490 |
| 660 | 2023660 | Pkc Phospho Site(177-179) |
| 661 | 2023661 | 7E-92 >gi 4056504 (AC005896) zinc finger protein [Arabidopsis thaliana] Length = 178 |
| 662 | 2023662 | Tyr Phospho Site(441-448) |
| 663 | 2023663 | Tyr Phospho Site(1407-1415) |
| 664 | 2023664 | 2E-60 >gi 1532175 (U63815) similar to protein disulfide isomerase [Arabidopsis thaliana] Length = 132 |
| 665 | 2023665 | 1E-128 >emb CAB10215.1 (Z97336) ankyrin like protein [Arabidopsis thaliana] Length = 936 |
| 666 | 2023666 | Tyr Phospho Site(764-772) |
| 667 | 2023667 | 1E-107 >emb CAB52747.1 (AJ245629) photosystem I subunit III precursor [Arabidopsis thaliana] Length = 221 |
| 668 | 2023668 | Tyr Phospho Site(146-152) |
| 669 | 2023669 | 1E-112 >gi 3065835 (AF058800) methyltransferase [Arabidopsis thaliana] Length = 504 |
| 670 | 2023670 | Tyr Phospho Site(910-918) |
| 671 | 2023671 | Tyr Phospho Site(1058-1064) |
| 672 | 2023672 | Tyr Phospho Site(377-383) |
| 673 | 2023673 | 2E-33 >gi 4097549 (U64907) ATPF4 [Arabidopsis thaliana] Length = 179 |
| 674 | 2023674 | 1E-119 >sp P41916 RAN1_ARATH GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi 495729 (L16789) small ras-related protein [Arabidopsis thaliana] >gi 2058278 emb CAA66047 (X97379) atran1 [Arabidopsis thaliana] Length = 221 |
| 675 | 2023675 | 1E-105 >sp P22953 HS71_ARATH HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi 397482 emb CAA52684 (X74604) heat shock protein 70 cognate [Arabidopsis thaliana] Length = 651 |
| 676 | 2023676 | 2E-89 >gb AAD39282.1 AC007576_5 (AC007576) Similar to DNA-binding proteins [Arabidopsis thaliana] Length = 487 |
| 677 | 2023677 | 1E-127 >gi 4056505 (AC005896) nodulin-like protein [Arabidopsis thaliana] Length = 357 |
| 678 | 2023678 | 1E-135 >gi 886116 (U27609) TCH4 protein [Arabidopsis thaliana] >gi 2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana] Length = 284 |
| 679 | 2023679 | 2E-90 >sp O23255 SAHH_ARATH ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi 2244750 emb CAB10173.1 (Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi 3088579 gb AAC14714.1 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana] Length = 485 |
| 680 | 2023680 | 9E-23 >dbj BAA32422 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana] Length = 300 |
| 681 | 2023681 | Tyr Phospho Site(304-312) |
| 682 | 2023682 | Tyr Phospho Site(654-660) |
| 683 | 2023683 | 2E-58 >sp Q43434 VATL_GOSHI VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi 4519415 dbj BAA75542.1 (AB024275) |

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| | | vacuolar H ⁺ -ATPase c subunit [Citrus unshiu] Length = 165 |
| 684 | 2023684 | 1E-106 >pir S50767 protein kinase - rice >gi 450300 (L27821) protein kinase [Oryza sativa] Length = 824 |
| 685 | 2023685 | 6E-14 >sp Q28891 S5A1_MACFA 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) >gi 999036 bbs 164548 (S77162) steroid 5 alpha-reductase type 1 isoenzyme, SR type 1 [Cynomolgus monkeys, prostate, Peptide, 263 aa] [Macaca fascicularis] Length = 263 |
| 686 | 2023686 | 1E-131 >gb AAC34217.1 (AC004411) alcohol dehydrogenase [Arabidopsis thaliana] Length = 257 |
| 687 | 2023687 | Tyr_Phospho_Site(146-152) |
| 688 | 2023688 | 2E-72 >emb CAB44322.1 (AL078606) phospholipase D-gamma [Arabidopsis thaliana] Length = 866 |
| 689 | 2023689 | 8E-97 >emb CAB53034.1 (AJ245867) photosystem I subunit XI precursor [Arabidopsis thaliana] Length = 219 |
| 690 | 2023690 | 1E-133 >sp O80585 MTHR_ARATH PROBABLE METHYLENETETRAHYDROFOLATE REDUCTASE >gi 3212869 (AC004005) unknown protein [Arabidopsis thaliana] Length = 606 |
| 691 | 2023691 | Tyr_Phospho_Site(501-508) |
| 692 | 2023692 | 6E-26 >gb AAD40017.1 AF150111_1 (AF150111) small zinc finger-like protein [Arabidopsis thaliana] Length = 93 |
| 693 | 2023693 | 1E-101) >gi 4056469 (AC005990) Strong similarity to gb M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb Z25826, gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967, gb AA712956, gb T46403, gb T46050, gb AI100391 and gb Z25043 come from t... Length = 188 |
| 694 | 2023694 | Zinc Protease(160-169) |
| 695 | 2023695 | 3E-94 >emb CAB36847.1 (AL035528) DnaJ-like protein [Arabidopsis thaliana] Length = 197 |
| 696 | 2023696 | Tyr_Phospho_Site(1062-1069) |
| 697 | 2023697 | 1E-83 >sp P35132 UBC9_ARATH UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi 421857 pir S32674 ubiquitin—protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] Length = 148 |
| 698 | 2023698 | 2E-47 >emb CAA09200 (AJ010461) RNA helicase [Arabidopsis thaliana] Length = 363 |
| 699 | 2023699 | Tyr_Phospho_Site(1315-1322) |
| 700 | 2023700 | 3E-86 >gb AAD22122.1 AC006224_4 (AC006224) isopropylmalate dehydratase [Arabidopsis thaliana] Length = 256 |
| 701 | 2023701 | 9E-11 >pir S59397 probable membrane protein YLR251w - yeast (Saccharomyces cerevisiae) >gi 662333 (U20865) Ylr251wp [Saccharomyces cerevisiae] Length = 197 |
| 702 | 2023702 | 1E-113 >sp O23755 EF2_BETVU ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900 (Z97178) elongation factor 2 [Beta vulgaris] Length = 843 |
| 703 | 2023703 | 8E-46 >pir A39634 probable cell cycle control protein crn - fruit fly (Drosophila melanogaster) >gi 2827496 emb CAA15705.1 (AL009195) EG:30B8.1 [Drosophila melanogaster] Length = 702 |
| 704 | 2023704 | Tyr_Phospho_Site(1307-1314) |
| 705 | 2023705 | 1E-145 >gb AAD46682.1 AF170910_1 (AF170910) SYNC2 protein [Arabidopsis thaliana] Length = 638 |
| 706 | 2023706 | 1E-65 >gi 3341698 (AC003672) blue copper-binding protein II |

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| | | [Arabidopsis thaliana] Length = 202 |
| 707 | 2023707 | Rgd(993-995) |
| 708 | 2023708 | Tyr Phospho Site(94-101) |
| 709 | 2023709 | Tyr Phospho Site(1050-1057) |
| 710 | 2023710 | 1E-107 >gb AAD39612.1 AC007454_11 (AC007454) Similar to gb X92204 NAM gene product from Petunia hybrida. ESTs gb H36656 and gb AA651216 come from this gene. [Arabidopsis thaliana] Length = 557 |
| 711 | 2023711 | 7E-88 >gb AAD27909.1 AC007213_7 (AC007213) receptor protein kinase [Arabidopsis thaliana] Length = 851 |
| 712 | 2023712 | 2E-89 >dbj BAA18577 (D90915) peptide chain release factor [Synechocystis sp.] Length = 288 |
| 713 | 2023713 | 4E-54 >gb AAD21451.1 (AC007017) DNA-binding protein [Arabidopsis thaliana] Length = 145 |
| 714 | 2023714 | Tyr Phospho Site(7-14) |
| 715 | 2023715 | Tyr Phospho Site(467-473) |
| 716 | 2023716 | Tyr Phospho Site(185-191) |
| 717 | 2023717 | 6E-48 >gb AAD39312.1 AC007258_1 (AC007258) Similar to glutathione transferase [Arabidopsis thaliana] Length = 234 |
| 718 | 2023718 | 8E-17 >sp Q42534 PME2_ARATH PECTINESTERASE 2 (PECTIN METHYLESTERASE 2) (PE 2) >gi 2129667 pir PC4168 pectinesterase (EC 3.1.1.11) 2 precursor - Arabidopsis thaliana (fragment) >gi 903894 (U25649) ATPME2 precursor [Arabidopsis thaliana] Length = 582 |
| 719 | 2023719 | Tyr Phospho Site(1205-1211) |
| 720 | 2023720 | Tyr Phospho Site(297-304) |
| 721 | 2023721 | 1E-103 >sp Q96252 ATP4_ARATH ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi 1655484 dbj BAA13601 (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] Length = 203 |
| 722 | 2023722 | 9E-59 >emb CAB39656.1 (AL049483) nitrogen fixation like protein [Arabidopsis thaliana] Length = 224 |
| 723 | 2023723 | 2E-27 >gi 2984333 (AE000774) Na(+) dependent transporter (Sbf family) [Aquifex aeolicus] Length = 297 |
| 724 | 2023724 | Tyr Phospho Site(780-786) |
| 725 | 2023725 | 2E-45 >gb AAD22286.1 AC006920_10 (AC006920) reverse transcriptase [Arabidopsis thaliana] Length = 1311 |
| 726 | 2023726 | 4E-44 >emb CAA63223 (X92491) TOM20 [Solanum tuberosum] Length = 204 |
| 727 | 2023727 | 1E-23 >emb CAB10456.1 (Z97342) nuclear antigen homolog [Arabidopsis thaliana] Length = 355 |
| 728 | 2023728 | 1E-82 >dbj BAA06384 (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis thaliana] Length = 163 |
| 729 | 2023729 | 6E-24 >gb AAD24601.1 AC005825_8 (AC005825) reverse transcriptase [Arabidopsis thaliana] Length = 1319 |
| 730 | 2023730 | 1E-36 >emb CAB16764.1 (Z99707) heat shock transcription factor HSF4 [Arabidopsis thaliana] >gi 3256070 emb CAA74398 (Y14069) Heat Shock Factor 4 [Arabidopsis thaliana] Length = 284 |
| 731 | 2023731 | 1E-68 >gb AAD25624.1 AC005287_26 (AC005287) Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana] Length = 535 |
| 732 | 2023732 | 1E-114 >gb AAD41426.1 AC007727_15 (AC007727) Identical to gb Y13173 Arabidopsis thaliana mRNA for proteasome subunit. EST gb T76747 comes from this gene. Length = 204 |
| 733 | 2023733 | 1E-105 >sp P41127 RL13_ARATH 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein |

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| | | [<i>Arabidopsis thaliana</i>] Length = 206 |
| 734 | 2023734 | Tyr_Phospho_Site(199-205) |
| 735 | 2023735 | 4E-41 >emb CAB44393.1 (AL078610) hydrolase [<i>Streptomyces coelicolor</i>] Length = 269 |
| 736 | 2023736 | 5E-29 >gb AAD56248.1 AF186273_1 (AF186273) leucine-rich repeats containing F-box protein FBL3 [<i>Homo sapiens</i>] Length = 423 |
| 737 | 2023737 | Tyr_Phospho_Site(1188-1195) |
| 738 | 2023738 | 5E-63 >gi 3834306 (AC005679) EST gb R65024 comes from this gene. [<i>Arabidopsis thaliana</i>] Length = 156 |
| 739 | 2023739 | 1E-78 >gi 1707018 (U78721) CutA isolog [<i>Arabidopsis thaliana</i>] Length = 182 |
| 740 | 2023740 | 1E-164 >gb AAD17364 (AF128396) <i>Arabidopsis thaliana</i> flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1) [<i>Arabidopsis thaliana</i>] Length = 702 |
| 741 | 2023741 | 9E-14 >ref NP_003913.1 PHERC1 guanine nucleotide exchange factor p532 >gi 1477565 (U50078) p532 [<i>Homo sapiens</i>] Length = 4861 |
| 742 | 2023742 | 1E-133 >emb CAA65053 (X95738) proline transporter 2 [<i>Arabidopsis thaliana</i>] Length = 439 |
| 743 | 2023743 | 6E-93 >gb AAD39312.1 AC007258_1 (AC007258) Similar to glutathione transferase [<i>Arabidopsis thaliana</i>] Length = 234 |
| 744 | 2023744 | Tyr_Phospho_Site(748-755) |
| 745 | 2023745 | 1E-120 >gb AAC24832 (AF061518) manganese superoxide dismutase [<i>Arabidopsis thaliana</i>] Length = 231 |
| 746 | 2023746 | 3E-83 >emb CAB45986.1 (AL080318) protein [<i>Arabidopsis thaliana</i>] Length = 206 |
| 747 | 2023747 | 3E-22 >gi 895613 (L43505) CASP gene product [<i>Gallus gallus</i>] Length = 675 |
| 748 | 2023748 | 4E-39 >gb AAD21699.1 (AC004793) Contains reverse transcriptase domain (rvt) PF 00078. [<i>Arabidopsis thaliana</i>] Length = 1253 |
| 749 | 2023749 | 1E-124 >emb CAA19720.1 (AL030978) GH3 like protein [<i>Arabidopsis thaliana</i>] Length = 612 |
| 750 | 2023750 | 1E-69 >emb CAB36546.1 (AL035440) DNA binding protein [<i>Arabidopsis thaliana</i>] Length = 427 |
| 751 | 2023751 | 3E-75 >gi 1707022 (U78721) proline-rich protein isolog [<i>Arabidopsis thaliana</i>] Length = 239 |
| 752 | 2023752 | 1E-122 >gb AAD17428 (AC006284) methyltransferase [<i>Arabidopsis thaliana</i>] Length = 619 |
| 753 | 2023753 | 3E-15 >gi 2252854 (AF013294) similar to auxin-induced protein [<i>Arabidopsis thaliana</i>] Length = 122 |
| 754 | 2023754 | 1E-101 >gi 2444176 (U94782) unconventional myosin [<i>Helianthus annuus</i>] Length = 1260 |
| 755 | 2023755 | Tyr_Phospho_Site(661-668) |
| 756 | 2023756 | 7E-97 >gb AAD15400 (AC006223) integral membrane protein [<i>Arabidopsis thaliana</i>] Length = 429 |
| 757 | 2023757 | 1E-120 >sp P42761 GTH3_ARATH GLUTATHIONE S-TRANSFERASE ERD13 (GST CLASS PHI) >gi 481822 pir S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - <i>Arabidopsis thaliana</i> >gi 497789 dbj BAA04554 (D17673) glutathio |
| 758 | 2023758 | 1E-114 >gi 1707015 (U78721) protein phosphatase 2C isolog [<i>Arabidopsis thaliana</i>] Length = 380 |
| 759 | 2023759 | 1E-108 >gb AAD24598.1 AC005825_5 (AC005825) chloroplast outer membrane protein 86, also very similar to GTP-binding protein from pea (GB:L36857) [<i>Arabidopsis thaliana</i>] Length = 1206 |
| 760 | 2023760 | 1E-82 >emb CAA16964 (AL021811) H ⁺ -transporting ATP synthase chain9 - like protein [<i>Arabidopsis thaliana</i>] >gi 5730141 emb CAB52473.1 |

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| | | (AJ245574) ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana] Length = 219 |
| 761 | 2023761 | 3E-47 >emb CAA68848 (Y07563) hin1 [Nicotiana tabacum] Length = 221 |
| 762 | 2023762 | 9E-51 >sp P28342 GTT1_DIACA GLUTATHIONE S-TRANSFERASE 1 (SR8) (GST CLASS-THETA) >gi 99589 pir S16604 glutathione transferase (EC 2.5.1.18) CARSR8 - clove pink >gi 18330 emb CAA41279 (X58390) glutathione s-transferase [Dianthus caryophyllus] >gi 167968 (M64268) glutathione transferase [Dianthus caryophyllus] Length = 221 |
| 763 | 2023763 | Tyr_Phospho_Site(192-199) |
| 764 | 2023764 | Tyr_Phospho_Site(1388-1396) |
| 765 | 2023765 | 1E-38 >emb CAB40579.1 (AJ133639) SAH7 protein [Arabidopsis thaliana] Length = 159 |
| 766 | 2023766 | 4E-17 >ref NP_003554.1 PSPPOP speckle-type POZ protein >gi 2695708 emb CAA04199 (AJ000644) SPOP [Homo sapiens] Length = 374 |
| 767 | 2023767 | Pkc_Phospho_Site(22-24) |
| 768 | 2023768 | 3E-31 >sp P81650 BGAL_PSBAT BETA-GALACTOSIDASE (LACTASE) >gi 4079639 emb CAA10470 (AJ131635) beta-galactosidase [psychrophilic bacterium TAE 79] Length = 1039 |
| 769 | 2023769 | 1E-123 >gi 871782 (L43081) pEARLI 4 gene product [Arabidopsis thaliana] Length = 766 |
| 770 | 2023770 | 2E-77 >gi 3386612 (AC004665) DNA-binding protein, dbp [Arabidopsis thaliana] Length = 190 |
| 771 | 2023771 | 1E-29 >sp P42763 DH14_ARATH DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14 protein [Arabidopsis thaliana] Length = 185 |
| 772 | 2023772 | 8E-13 >emb CAA88860.1 (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk3... Length = 556 |
| 773 | 2023773 | 1E-107 >gb AAC34243.1 (AC004411) pto kinase [Arabidopsis thaliana] Length = 365 |
| 774 | 2023774 | 9E-88 >gi 3075394 (AC004484) beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead protein [Arabidopsis thaliana] Length = 550 |
| 775 | 2023775 | Tyr_Phospho_Site(428-434) |
| 776 | 2023776 | 1E-125 >emb CAB45880.1 (AL080282) protein [Arabidopsis thaliana] Length = 1396 |
| 777 | 2023777 | 5E-73 >sp P52810 RS9_PODAN 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433 (X96613) cytoplasmic ribosomal protein S7 [Podospira anserina] Length = 190 |
| 778 | 2023778 | 1E-138 >gi 1066499 (L37606) NADH-dependent glutamate synthase [Medicago sativa] Length = 2194 |
| 779 | 2023779 | 4E-37 >gb AAD19788 (AC006528) zinc-finger protein, 5' partial [Arabidopsis thaliana] Length = 626 |
| 780 | 2023780 | 1E-10 >gi 3600032 (AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana] Length = 466 |
| 781 | 2023781 | 9E-86 >gi 2924779 (AC002334) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi 2981616 dbj BAA25248 (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi 2981618 dbj BAA25249 (AB008855) 3-ketoacyl |
| 782 | 2023782 | 2E-91 >emb CAB16762.1 (Z99707) caltractin-like protein [Arabidopsis thaliana] Length = 167 |
| 783 | 2023783 | 3E-50 >gb AAD21025 (AF106939) 1,4-benzoquinone reductase [Phanerochaete chrysosporium] Length = 201 |
| 784 | 2023784 | Tyr_Phospho_Site(1296-1304) |

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| 785 | 2023785 | Tyr Phospho Site(290-296) |
| 786 | 2023786 | 2E-52 >gb AAD22344.1 AC006592_1 (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase, 3' partial [Arabidopsis thaliana] Length = 414 |
| 787 | 2023787 | Tyr Phospho Site(49-56) |
| 788 | 2023788 | 1E-70 >emb CAB41005.1 (AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana] Length = 141 |
| 789 | 2023789 | 8E-25 >sp P73689 SPPA_SYNY3 PROTEASE IV HOMOLOG (ENDOPEPTIDASE IV) >gi 1652816 dbj BAA17735 (D90908) protease IV [Synechocystis sp.] Length = 610 |
| 790 | 2023790 | 1E-120 >sp Q42599 NUIM_ARATH NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi 1076356 pir S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi 666977 emb CAA59061 (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi 3152573 |
| 791 | 2023791 | 4E-91 >gb AAD44761.1 AF144752_1 (AF144752) 40S ribosomal protein S7 homolog [Brassica oleracea] Length = 191 |
| 792 | 2023792 | 1E-121 >pir S36884 ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana] Length = 591 |
| 793 | 2023793 | Pkc Phospho Site(29-31) |
| 794 | 2023794 | 8E-53 >gi 4220474 (AC006069) myosin heavy chain [Arabidopsis thaliana] Length = 629 |
| 795 | 2023795 | 1E-140 >sp O64637 C7C2_ARATH CYTOCHROME P450 76C2 >gi 2979549 (AC003680) 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana] Length = 512 |
| 796 | 2023796 | 1E-77 >emb CAA96435 (Z71753) pectin methylesterase [Nicotiana plumbaginifolia] Length = 315 |
| 797 | 2023797 | 4E-79 >emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana] Length = 263 |
| 798 | 2023798 | 3E-27 >ref NP_006818.1 PTMP21 transmembrane trafficking protein >gi 3915893 sp P49755 TM21_HUMAN TRANSMEMBRANE PROTEIN TMP21 PRECURSOR (S3111125) (S311125) >gi 1359886 emb CAA66071 (X97442) transmembrane protein [Homo sapiens] >gi 1407826 (U61734) protein trafficking protein [Homo sapiens] >gi 3288463 emb CAA06213.1 (AJ004913) integral membrane protein, Tmp21-l (p23) [Homo sapiens] >gi 4885697 gb AAD31941.1 AC007055_6 (AC007055) TMP21 [Homo sapiens] Length = 219 |
| 799 | 2023799 | Tyr Phospho Site(250-257) |
| 800 | 2023800 | 8E-19 >gi 3193325 (AF069299) contains similarity to pectinesterases [Arabidopsis thaliana] Length = 209 |
| 801 | 2023801 | Tyr Phospho Site(236-242) |
| 802 | 2023802 | 1E-147 >emb CAB41122.1 (AL049657) proteasome regulatory subunit [Arabidopsis thaliana] Length = 406 |
| 803 | 2023803 | 2E-49 >emb CAB00039.1 (Z75712) Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST EMBL:Z14470 comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST yk482d4.5 comes from this gene [Caenorhabditis elegans] Length = 405 |
| 804 | 2023804 | 3E-77 >emb CAB38828.1 (AL035679) proton pump [Arabidopsis thaliana] Length = 843 |
| 805 | 2023805 | Pkc Phospho Site(74-76) |
| 806 | 2023806 | Pkc Phospho Site(147-149) |
| 807 | 2023807 | 2E-97 >sp P49177 GBB_ARATH GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi 557694 (U12232) GTP binding protein beta subunit [Arabidopsis thaliana] >gi 3096915 emb CAA18825.1 (AL023094) GTP binding protein beta subunit [A |
| 808 | 2023808 | 2E-79 >dbj BAA13947 (D89341) luminal binding protein [Arabidopsis |

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| | | thaliana] Length = 669 |
| 809 | 2023809 | 5E-79 >emb CAA73063.1 (Y12459) cytosolic glutamine synthetase [Brassica napus] Length = 356 |
| 810 | 2023810 | 1E-82 >sp P29525 OLEO_ARATH OLEOSIN >gi 282875 pir S22538 oleosin - Arabidopsis thaliana >gi 16405 emb CAA44225 (X62353) oleosin [Arabidopsis thaliana] >gi 4455257 emb CAB36756.1 (AL035523) oleosin, 18.5K [Arabidopsis thaliana] Length = 356 |
| 811 | 2023811 | 1E-108 >gi 4056502 (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana] Length = 207 |
| 812 | 2023812 | 1E-123 >gi 3319357 (AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana] Length = 662 |
| 813 | 2023813 | 7E-55 >emb CAB06417 (Z84377) xylosidase [Aspergillus niger] Length = 804 |
| 814 | 2023814 | 3E-11 >gi 3548810 (AC005313) chloroplast nucleoid DNA binding protein [Arabidopsis thaliana] Length = 461 |
| 815 | 2023815 | 3E-33 >gi 3402683 (AC004697) patatin-like protein [Arabidopsis thaliana] Length = 499 |
| 816 | 2023816 | 6E-92 >sp P49209 RL9_ARATH 60S RIBOSOMAL PROTEIN L9 >gi 2129720 pir S71255 ribosomal protein L9 - Arabidopsis thaliana >gi 1107489 emb CAA63024 (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana] Length = 195 |
| 817 | 2023817 | 1E-10 >emb CAB38212 (AL035601) protein [Arabidopsis thaliana] Length = 252 |
| 818 | 2023818 | 1E-130 >gi 2618688 (AC002510) esterase D [Arabidopsis thaliana] Length = 284 |
| 819 | 2023819 | 1E-171 >sp P46644 AAT3_ARATH ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi 693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana] Length = 449 |
| 820 | 2023820 | 1E-17 >dbj BAA33206 (AB001888) zinc finger protein [Oryza sativa] Length = 407 |
| 821 | 2023821 | Tyr_Phospho_Site(160-167) |
| 822 | 2023822 | 1E-122 >gi 2388578 (AC000098) Similar to Mycobacterium RlpF (gb Z84395). ESTs gb T75785,gb R30580,gb T04698 come from this gene. [Arabidopsis thaliana] Length = 223 |
| 823 | 2023823 | 1E-129 >gb AAD25665.1 AC007020_7 (AC007020) ferritin protein [Arabidopsis thaliana] >gi 4588004 gb AAD25945.1 AF085279_18 (AF085279) hypothetical ferritin subunit [Arabidopsis thaliana] Length = 259 |
| 824 | 2023824 | Zinc Finger C2h2(360-382) |
| 825 | 2023825 | 2E-91 >gi 3688799 (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana] Length = 253 |
| 826 | 2023826 | Tyr_Phospho_Site(60-67) |
| 827 | 2023827 | 6E-68 >sp P32110 GTX6_SOYBN PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi 99912 pir A33654 heat shock protein 26A - soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max] Length = 225 |
| 828 | 2023828 | 1E-101 >gb AAD39666.1 AC007591_31 (AC007591) Is a member of the PF00903 glyoxalase family. ESTs gb T44721, gb T21844 and gb AA395404 come from this gene. [Arabidopsis thaliana] Length = 174 |
| 829 | 2023829 | Rgd(1357-1359) |
| 830 | 2023830 | 5E-90 >gb AAD30232.1 AC007202_14 (AC007202) Is a member of the PF00171 aldehyde dehydrogenase family. ESTs gb T21534, gb N65241 and gb AA395614 come from this gene. [Arabidopsis thaliana] Length = 509 |
| 831 | 2023831 | 2E-20 >sp Q46036 BLC_CITFR OUTER MEMBRANE LIPOPROTEIN BLC |

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| | | PRECURSOR >gi 2121019 pir 40710 outer membrane lipoprotein - Citrobacter freundii >gi 717136 (U21727) lipocalin precursor [Citrobacter freundii] Length = 177 |
| 832 | 2023832 | 2E-89 >sp P30707 RL9_PEA 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9 - garden pea >gi 20727 emb CAA46273 (X65155) GA [Pisum sativum] Length = 193 |
| 833 | 2023833 | Tyr_Phospho_Site(896-903) |
| 834 | 2023834 | 2E-87 >sp P42748 UBC4_ARATH UBIQUITIN-CONJUGATING ENZYME E2-21 KD 1 (UBIQUITIN-PROTEIN LIGASE 4) (UBIQUITIN CARRIER PROTEIN 4) >gi 431266 (L19354) ubiquitin conjugating enzyme [Arabidopsis thaliana] Length = 187 |
| 835 | 2023835 | 9E-83 >gi 1256424 (U51119) cysteine proteinase inhibitor [Brassica campestris] Length = 205 |
| 836 | 2023836 | 1E-119 >gb AAD50015.1 AC007651_10 (AC007651) glutathione transferase [Arabidopsis thaliana] Length = 221 |
| 837 | 2023837 | Zinc_Finger_C2h2(1242-1265) |
| 838 | 2023838 | Tyr_Phospho_Site(88-96) |
| 839 | 2023839 | Pkc_Phospho_Site(31-33) |
| 840 | 2023840 | 1E-180 >gi 3355490 (AC004218) dolichyl-phosphate beta-glucosyltransferase [Arabidopsis thaliana] Length = 336 |
| 841 | 2023841 | 1E-101 >gi 682728 (L40031) S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana] Length = 212 |
| 842 | 2023842 | 3E-14 >gi 3293547 (AF072709) oxidoreductase [Streptomyces lividans] Length = 313 |
| 843 | 2023843 | 5E-25 >dbj BAA82843.1 (AB023651) miraculin homologue [Solanum melongena] Length = 160 |
| 844 | 2023844 | 1E-110 >sp P54888 P5C2_ARATH DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [INCLUDES: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi 887388 emb CAA60447 (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi 1669658 emb CAA70527 (Y09355) pyrroline-5-carboxylate synthetase [Arabidopsis thaliana] Length = 726 |
| 845 | 2023845 | 1E-138 >gi 1020155 (U26936) DNA-binding protein [Arabidopsis thaliana] Length = 236 |
| 846 | 2023846 | 4E-76 >emb CAB38956.1 (AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana] Length = 500 |
| 847 | 2023847 | 1E-155 >gi 4185136 (AC005724) trehalose-6-phosphate synthase [Arabidopsis thaliana] Length = 862 |
| 848 | 2023848 | 1E-30 >gi 2642215 (AF030386) NOI protein [Arabidopsis thaliana] Length = 79 |
| 849 | 2023849 | 2E-59 >gi 2739044 (AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max] Length = 324 |
| 850 | 2023850 | 2E-59 >sp P40602 APG_ARATH ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi 99694 pir S21961 proline-rich protein APG - Arabidopsis thaliana >gi 22599 emb CAA42925 (X60377) APG [Arabidopsis thaliana] Length = 534 |
| 851 | 2023851 | Pkc_Phospho_Site(5-7) |
| 852 | 2023852 | 1E-104 >gi 3395434 (AC004683) peroxidase [Arabidopsis thaliana] >gi 742248 prf 2009327B peroxidase [Arabidopsis thaliana] Length = 349 |
| 853 | 2023853 | Tyr_Phospho_Site(1115-1122) |
| 854 | 2023854 | 6E-40 >dbj BAA76393.1 (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa] Length = 169 |
| 855 | 2023855 | Tyr_Phospho_Site(426-433) |

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| 856 | 2023856 | 6E-43 >pir S52995 arabinogalactan-like protein - loblolly pine >gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda] Length = 264 |
| 857 | 2023857 | 3E-91 >sp P47997 G11A_ORYSA PROTEIN KINASE G11A >gi 100705 pir B30311 protein kinase C (EC 2.7.1.-) homolog - rice (fragment) >gi 169788 (J04556) G11A protein [Oryza sativa] Length = 531 |
| 858 | 2023858 | 3E-93 >gi 3927825 (AC005727) dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] Length = 343 |
| 859 | 2023859 | 1E-101 >gb AAD41971.1 AC006438_3 (AC006438) cold acclimation protein WCOR413 [Triticum aestivum] [Arabidopsis thaliana] Length = 197 |
| 860 | 2023860 | 1E-137 >emb CAB37533 (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana] Length = 517 |
| 861 | 2023861 | 1E-112 >gi 4056502 (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana] Length = 207 |
| 862 | 2023862 | 6E-98 >gi 4204274 (AC004146) ribulose biphosphate carboxylase, small subunit [Arabidopsis thaliana] Length = 180 |
| 863 | 2023863 | 4E-76 >pir S71286 oleosin isoform - Arabidopsis thaliana >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin [Arabidopsis thaliana] Length = 191 |
| 864 | 2023864 | Pkc Phospho Site(42-44) |
| 865 | 2023865 | Tyr Phospho Site(974-982) |
| 866 | 2023866 | Tyr Phospho Site(355-362) |
| 867 | 2023867 | 6E-35 >dbj BAA18248 (D90912) ferredoxin [Synechocystis sp.] Length = 122 |
| 868 | 2023868 | Tyr Phospho Site(109-117) |
| 869 | 2023869 | Tyr Phospho Site(638-645) |
| 870 | 2023870 | 5E-30 >emb CAB55502.1 (AJ131768) tyramine hydroxycinnamoyltransferase [Nicotiana tabacum] Length = 226 |
| 871 | 2023871 | 1E-131 >emb CAB45850.1 (AL080254) reticuline oxidase-like protein [Arabidopsis thaliana] Length = 539 |
| 872 | 2023872 | 9E-99 >emb CAB41123.1 (AL049657) argininosuccinate synthase-like protein [Arabidopsis thaliana] Length = 498 |
| 873 | 2023873 | Tyr Phospho Site(1364-1370) |
| 874 | 2023874 | 1E-108 >gb AAD32833.1 AC007659_15 (AC007659) mitochondrial elongation factor G [Arabidopsis thaliana] Length = 754 |
| 875 | 2023875 | 1E-66 >emb CAA65533 (X96758) clathrin coat assembly protein AP17 [Zea mays] Length = 132 |
| 876 | 2023876 | 3E-92 >sp Q43117 KPYA_RICCO PYRUVATE KINASE ISOZYME A, CHLOROPLAST PRECURSOR >gi 169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis] Length = 583 |
| 877 | 2023877 | 4E-83 >emb CAB10235.1 (Z97336) auxin-responsive protein IAA1 [Arabidopsis thaliana] Length = 168 |
| 878 | 2023878 | 2E-33 >gi 3822225 (AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana] Length = 190 |
| 879 | 2023879 | 1E-24 >gb AAD38289.1 AC007789_15 (AC007789) ABA induced plasma membrane protein [Oryza sativa] Length = 189 |
| 880 | 2023880 | 1E-105 >sp P10797 RBS3_ARATH RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701 (X14564) ribulose biphosphate carboxylase [Arabidopsis thaliana] Length = 181 |
| 881 | 2023881 | 1E-139 >gi 3402678 (AC004697) adenylate kinase [Arabidopsis thaliana] Length = 295 |
| 882 | 2023882 | Tyr Phospho Site(98-106) |
| 883 | 2023883 | 5E-26 >gb AAD34267.1 AF084419_1 (AF084419) calmodulin mutant SYNCAM64A [synthetic construct] Length = 147 |

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| 884 | 2023884 | 2E-15 >bbs 48073 13 kDa-B polypeptide of iron-sulfur protein fraction of NADH:ubiquinone oxidoreductase [cattle, heart, Peptide Mitochondrial Partial, 114 aa] Length = 114 |
| 885 | 2023885 | Tyr_Phospho_Site(937-944) |
| 886 | 2023886 | 4E-73 >gb AAD39281.1 AC007576_4 (AC007576) initiation factor 5A-4 [Arabidopsis thaliana] Length = 158 |
| 887 | 2023887 | Pkc_Phospho_Site(69-71) |
| 888 | 2023888 | Tyr_Phospho_Site(100-106) |
| 889 | 2023889 | 6E-74 >emb CAB38706.1 (AJ131464) nitrate transporter [Arabidopsis thaliana] Length = 567 |
| 890 | 2023890 | Tyr_Phospho_Site(1268-1275) |
| 891 | 2023891 | Zinc_Finger_C2h2(755-775) |
| 892 | 2023892 | 7E-81 >dbj BAA24074 (D89824) GTP-binding protein [Arabidopsis thaliana] Length = 210 |
| 893 | 2023893 | 2E-33 >gi 4164539 (AF079170) phloem protein [Cucurbita maxima] Length = 150 |
| 894 | 2023894 | 4E-15 >gi 2739366 (AC002505) SF16 like protein [Arabidopsis thaliana] Length = 516 |
| 895 | 2023895 | Phospho_Site(1301-1307) |
| 896 | 2023896 | 1E-57 >emb CAA74052 (Y13724) Transcription factor [Arabidopsis thaliana] Length = 187 |
| 897 | 2023897 | Tyr_Phospho_Site(768-775) |
| 898 | 2023898 | 5E-38 >gi 3599491 (AF085149) aminotransferase [Capsicum chinense] Length = 459 |
| 899 | 2023899 | Rgd(210-212) |
| 900 | 2023900 | Tyr_Phospho_Site(1201-1208) |
| 901 | 2023901 | 1E-144 >pir S51697 oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi 2129530 pir S69195 acyl-(acyl carrier protein) thioesterase (clone TE 1-1) - Arabidopsis thaliana >gi 634003 emb CAA85387 (Z36910) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana] Length = 412 |
| 902 | 2023902 | 5E-79 >gi 2281629 (AF003095) AP2 domain containing protein RAP2.2 [Arabidopsis thaliana] Length = 246 |
| 903 | 2023903 | 5E-91 >sp Q39836 GBLP_SOYBN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 1256608 gb AAB05941.1 (U44850) G beta-like protein [Glycine max] Length = 325 |
| 904 | 2023904 | 7E-87 >gi 1872544 (U89014) early light-induced protein; ELIP [Arabidopsis thaliana] Length = 195 |
| 905 | 2023905 | 1E-108 >gi 507164 (U04818) PITSLRE alpha 2-4 [Homo sapiens] Length = 562 |
| 906 | 2023906 | 1E-121 >gi 3421082 (AF043523) 20S proteasome subunit PAD2 [Arabidopsis thaliana] Length = 250 |
| 907 | 2023907 | 6E-69 >sp P55964 KPYG_RICCO PYRUVATE KINASE ISOZYME G, CHLOROPLAST Length = 418 |
| 908 | 2023908 | 1E-108 >gi 3033400 (AC004238) Ser/Thr protein kinase [Arabidopsis thaliana] Length = 1257 |
| 909 | 2023909 | 1E-127 >gb AAD31337.1 AC007354_10 (AC007354) Strong similarity to gb Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF01326 Pyruvate phosphate dikinase, PEP/pyruvate binding domain. EST gb N96757 comes from this gene. [... Length = 1358 |
| 910 | 2023910 | Tyr_Phospho_Site(1347-1355) |
| 911 | 2023911 | Tyr_Phospho_Site(1324-1331) |
| 912 | 2023912 | Rgd(731-733) |
| 913 | 2023913 | 5E-31 >gb AAD20708 (AC006300) glucose-induced repressor protein [Arabidopsis thaliana] Length = 628 |

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| 914 | 2023914 | Tyr_Phospho_Site(4-11) |
| 915 | 2023915 | 3E-30 >emb CAB38807.1 (AL035678) nucellin-like protein [Arabidopsis thaliana] Length = 420 |
| 916 | 2023916 | 3E-50 >dbj BAA22813 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] Length = 502 |
| 917 | 2023917 | 5E-67 >gi 2281633 (AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana] Length = 229 |
| 918 | 2023918 | 2E-98 RBS4_ARATH RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN SUBUNIT |
| 919 | 2023919 | Sugar_Transport_2(364-389) |
| 920 | 2023920 | Tyr_Phospho_Site(218-225) |
| 921 | 2023921 | 3E-41 >emb CAB51834.1 (AJ243961) contains eukaryotic protein kinase domain PF 00069 [Oryza sativa] Length = 844 |
| 922 | 2023922 | 4E-28 >gb AAD28599.1 AF126742_1 (AF126742) bundle sheath defective protein 2 [Zea mays] Length = 129 |
| 923 | 2023923 | 2E-75 >gi 1408473 (U48939) actin depolymerizing factor 2 [Arabidopsis thaliana] Length = 137 |
| 924 | 2023924 | 1E-91 >dbj BAA20084.1 (AB003590) sulfate transporter [Arabidopsis thaliana] >gi 2114106 dbj BAA20085.1 (AB003591) sulfate transporter [Arabidopsis thaliana] Length = 677 |
| 925 | 2023925 | 5E-88 >gi 2317912 (U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana] Length = 357 |
| 926 | 2023926 | Tyr_Phospho_Site(591-597) |
| 927 | 2023927 | 1E-110 >emb CAA16940.1 (AL021768) small GTP-binding protein-like [Arabidopsis thaliana] Length = 200 |
| 928 | 2023928 | 1E-112 >gb AAD28774.1 AF134127_1 (AF134127) Lhcb4.2 protein [Arabidopsis thaliana] Length = 287 |
| 929 | 2023929 | 4E-54 >emb CAB56149.1 (AJ242970) BTF3b-like factor [Arabidopsis thaliana] Length = 165 |
| 930 | 2023930 | 5E-21 >gb AAD46412.1 AF096262_1 (AF096262) ER6 protein [Lycopersicon esculentum] Length = 168 |
| 931 | 2023931 | 1E-105 >sp P10797 RBS3_ARATH RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701 (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana] Length = 181 |
| 932 | 2023932 | Tyr_Phospho_Site(1153-1159) |
| 933 | 2023933 | 2E-82 >gi 3834310 (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb D83004 from Homo sapiens. ESTs gb T88233, gb Z24464, gb N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122 come from this gene. [Arabidopsis thaliana] Length = 163 |
| 934 | 2023934 | 1E-104 >gb AAB51571.1 (U75193) germin-like protein [Arabidopsis thaliana] >gi 1755168 gb AAB51573.1 (U75195) germin-like protein [Arabidopsis thaliana] >gi 2239042 emb CAA73213 (Y12673) GLP3 protein [Arabidopsis thaliana] Length = 206 |
| 935 | 2023935 | Tyr_Phospho_Site(1372-1379) |
| 936 | 2023936 | 1E-106 >emb CAB41927.1 (AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana] Length = 206 |
| 937 | 2023937 | Pkc_Phospho_Site(51-53) |
| 938 | 2023938 | 3E-79 >sp O65788 C7B2_ARATH CYTOCHROME P450 71B2 >gi 3164140 dbj BAA28537 (D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana] Length = 502 |
| 939 | 2023939 | Tyr_Phospho_Site(11-18) |
| 940 | 2023940 | Tyr_Phospho_Site(13-20) |
| 941 | 2023941 | 6E-57 >pir S52578 protein-serine/threonine kinase NPK15 - common tobacco >gi 505146 dbj BAA06538 (D31737) protein-serine/threonine kinase |

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| | | [<i>Nicotiana tabacum</i>] Length = 422 |
| 942 | 2023942 | 8E-94) >gi 3337356 (AC004481) protein transport protein SEC61 alpha subunit [<i>Arabidopsis thaliana</i>] Length = 475 |
| 943 | 2023943 | 4E-38 >gi 2459440 (AC002332) receptor kinase [<i>Arabidopsis thaliana</i>] Length = 664 |
| 944 | 2023944 | 6E-14 >sp P80728 MAVI_CUCPE MAVICYANIN >gi 1836088 bbs 179249 mavicyanin=12.752 kda small blue copper-containing stellacyanin-like glycoprotein/type I cupredoxin [<i>Cucurbita pepo</i> =green zucchini, peelings, Peptide, 108 aa] Length = 108 |
| 945 | 2023945 | 5E-60 >gb AAD34695.1 AC006341_23 (AC006341) Similar to gb AJ224359 surfet locus protein 5 (surf5b) from <i>Homo sapiens</i> . [<i>Arabidopsis thaliana</i>] Length = 150 |
| 946 | 2023946 | Tyr_Phospho_Site(257-264) |
| 947 | 2023947 | 1E-78) >emb CAB10195.1 (Z97335) transport protein [<i>Arabidopsis thaliana</i>] Length = 769 |
| 948 | 2023948 | 1E-39 >gi 3386612 (AC004665) DNA-binding protein, dbp [<i>Arabidopsis thaliana</i>] Length = 190 |
| 949 | 2023949 | Pkc_Phospho_Site(12-14) |
| 950 | 2023950 | Tyr_Phospho_Site(574-580) |
| 951 | 2023951 | 1E-55 >pir S37101 ATAF1 protein - <i>Arabidopsis thaliana</i> (fragment) >gi 1345506 emb CAA52771 (X74755) ATAF1 [<i>Arabidopsis thaliana</i>] Length = 229 |
| 952 | 2023952 | Pkc_Phospho_Site(45-47) |
| 953 | 2023953 | 1E-125 >emb CAB38921.1 (AL035709) bZIP transcription factor-like protein [<i>Arabidopsis thaliana</i>] Length = 305 |
| 954 | 2023954 | 1E-93 >emb CAA72792 (Y12071) thylakoid lumen rotamase [<i>Spinacia oleracea</i>] Length = 449 |
| 955 | 2023955 | 7E-64) >gi 2708746 (AC003952) DnaJ-like chaperonin [<i>Arabidopsis thaliana</i>] Length = 160 |
| 956 | 2023956 | 9E-95 >pir S33612 isocitrate dehydrogenase - soybean Length = 451 |
| 957 | 2023957 | 1E-106 >sp O23515 RL15_ARATH 60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447.1 (Z97341) ribosomal protein [<i>Arabidopsis thaliana</i>] Length = 204 |
| 958 | 2023958 | 1E-63 >gb AAC28488.1 (AF079588) 1-aminocyclopropane-1-carboxylate oxidase [<i>Sorghum bicolor</i>] Length = 316 |
| 959 | 2023959 | 3E-58 >emb CAB36546.1 (AL035440) DNA binding protein [<i>Arabidopsis thaliana</i>] Length = 427 |
| 960 | 2023960 | Tyr_Phospho_Site(190-196) |
| 961 | 2023961 | Tyr_Phospho_Site(818-825) |
| 962 | 2023962 | 1E-131 >gi 2511725 (AF021937) catalase 1 [<i>Arabidopsis thaliana</i>] Length = 492 |
| 963 | 2023963 | 1E-19 >gi 1905887 (U92461) recombination factor GdRad54 [<i>Gallus gallus</i>] Length = 733 |
| 964 | 2023964 | 1E-103 >sp P46283 S17P_ARATH SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi 1076403 pir S51838 sedoheptulose-1,7-biphosphatase - <i>Arabidopsis thaliana</i> >gi 786 |
| 965 | 2023965 | 2E-17 >emb CAA99819.1 (Z75533) waek similarty with bacillus amyloliquefaciens permease IIBC (Swiss Prot accession number P41029); cDNA EST yk573h3.3 comes from this gene [<i>Caenorhabditis elegans</i>] Length = 378 |
| 966 | 2023966 | 8E-26 >pir S49463 chloroplast RNA binding protein - kidney bean >gi 558629 emb CAA57551 (X82030) chloroplast RNA binding protein [<i>Phaseolus vulgaris</i>] Length = 287 |
| 967 | 2023967 | 1E-44 >emb CAA55397 (X78820) casein kinase I [<i>Arabidopsis thaliana</i>] Length = 364 |

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| 968 | 2023968 | 1E-105) >gb AAB51565.1 (U75187) germin-like protein [Arabidopsis thaliana] Length = 204 |
| 969 | 2023969 | 2E-96 >emb CAA65502 (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum] Length = 364 |
| 970 | 2023970 | Pkc_Phospho_Site(26-28) |
| 971 | 2023971 | 4E-43 >gi 871780 (L43080) pEARLI 1 gene product [Arabidopsis thaliana] >gi 4725947 emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana] Length = 168 |
| 972 | 2023972 | 2E-16 >sp P24805 TSJT_TOBAC STEM-SPECIFIC PROTEIN TSJT1 >gi 100383 pir S13551 stem-specific protein - common tobacco >gi 20037 emb CAA36525 (X52283) stem specific, weakly expressed in other organs [Nicotiana tabacum] Length = 149 |
| 973 | 2023973 | 1E-18 >gb AAD21041 (AF116237) pseudouridine synthase 1 [Mus musculus] Length = 393 |
| 974 | 2023974 | Tyr_Phospho_Site(95-102) |
| 975 | 2023975 | 1E-108) >prf 1804333B Gln synthetase [Arabidopsis thaliana] Length = 430 |
| 976 | 2023976 | 1E-116 >gi 2947070 (AC002521) Ser/Thr protein kinase [Arabidopsis thaliana] Length = 429 |
| 977 | 2023977 | 3E-15 >sp P74523 YE19_SYNY3 HYPOTHETICAL 17.7 KD PROTEIN SLR1419 >gi 1653717 dbj BAA18628 (D90916) hypothetical protein [Synechocystis sp.] Length = 159 |
| 978 | 2023978 | 7E-20 >gi 3033400 (AC004238) Ser/Thr protein kinase [Arabidopsis thaliana] Length = 1257 |
| 979 | 2023979 | Tyr_Phospho_Site(28-35) |
| 980 | 2023980 | Pkc_Phospho_Site(16-18) |
| 981 | 2023981 | Rgd(231-233) |
| 982 | 2023982 | Pkc_Phospho_Site(16-18) |
| 983 | 2023983 | 3E-24 >gi 2854070 (AF044914) histone deacetylase [Arabidopsis thaliana] Length = 305 |
| 984 | 2023984 | 1E-28 >gi 3157924 (AC002131) Contains homology to extensin-like protein gb D83227 from Populus nigra. ESTs gb H76425, gb T13883, gb T45348, gb H37743, gb AA042634, gb Z26960 and gb Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi 4063707 (AF104327) extensin-like protein [Arabidopsis thaliana] Length = 137 |
| 985 | 2023985 | Receptor_Cytokines_1(1550-1562) |
| 986 | 2023986 | 1E-113 >gi 3420055 (AC004680) cyclophilin [Arabidopsis thaliana] Length = 201 |
| 987 | 2023987 | 2E-27 >emb CAB45075.1 (AL078637) serine/threonine kinase-like protein [Arabidopsis thaliana] Length = 445 |
| 988 | 2023988 | Zinc_Finger_C2h2(929-950) |
| 989 | 2023989 | 1E-141 >pir S37495 peroxidase (EC 1.11.1.7) - Arabidopsis thaliana >gi 405611 emb CAA50677 (X71794) peroxidase [Arabidopsis thaliana] Length = 353 |
| 990 | 2023990 | Tyr_Phospho_Site(1189-1197) |
| 991 | 2023991 | 5E-92 >sp P28148 TF22_ARATH TRANSCRIPTION INITIATION FACTOR TFIID-2 (TATA-BOX FACTOR 2) (TATA SEQUENCE-BINDING PROTEIN 2) (TBP-2) >gi 99764 pir S10945 transcription initiation factor IID (clone At-1) - Arabidopsis thaliana >gi 16546 emb CAA38742 (X54995) transcription initiation factor II [Arabidopsis thaliana] >gi 4204264 (AC005223) 43453 [Arabidopsis thaliana] >gi 227073 prf 1613452A transcription initiation factor TFIID-1 [Arabidopsis thaliana] Length = 200 |
| 992 | 2023992 | 3E-16 >gi 3790581 (AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana] Length = 190 |
| 993 | 2023993 | 1E-20 >sp Q28735 TM21_RABIT TRANSMEMBRANE PROTEIN TMP21 |

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| | | PRECURSOR (INTEGRAL MEMBRANE PROTEIN P23) >gi 1370279 emb CAA66947 (X98303) transmembrane protein [Oryctolagus cuniculus] Length = 219 |
| 994 | 2023994 | Tyr_Phospho_Site(112-119) |
| 995 | 2023995 | 3E-11 >gb AAD35009.1 AF144391_1 (AF144391) thioredoxin-like 5 [Arabidopsis thaliana] Length = 185 |
| 996 | 2023996 | Tyr_Phospho_Site(1372-1379) |
| 997 | 2023997 | 7E-12 >sp P40389 UV22_SCHPO UV-INDUCED PROTEIN UVI22 >gi 629909 pir S47147 uvi22 protein - fission yeast (Schizosaccharomyces pombe) >gi 1076930 pir JC2442 UV inducible protein, UV122 - fission yeast (Schizosaccharomyces pombe) >gi 499199 emb CAA84069 (Z34299) uvi22 [Schizosaccharomyces pombe] >gi 3184086 emb CAA19342 (AL023781) uv-induced protein uvi22 [Schizosaccharomyces pombe] Length = 303 |
| 998 | 2023998 | 2E-28 >sp P30185 DH18_ARATH DEHYDRIN RAB18 >gi 282880 pir S28021 rab18 protein - Arabidopsis thaliana >gi 16451 emb CAA48178 (X68042) RAB18 [Arabidopsis thaliana] Length = 186 |
| 999 | 2023999 | 4E-93 >sp P42795 R111_ARATH 60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395 (X81799) ribosomal protein L16 [Arabidopsis thaliana] Length = 182 |